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### Method 1: Protein Source, using SW Model

50%: 00:14:41:37	Search time 15.84 seconds
July 12, 2002	(without alignments)
	569,909 Million cell updates/sec

15-18-826-441A-1

Sequences: 1. V.I.I.I.I.F.A.H.P.P.H.V.I.S.K.P.S.A. . . . . "K.N.V.V.V.V.I.O.I.I.I.F.M.I.N.A.H.V.I. 234

# Stiffness and Strength of H-Beam Columns

 $\text{diffcoef}(10,0)$ ,  $\text{diffcoef}(0,5)$ 

Residues 16,24-5015, 1871-5015 residues

Total number of hits and citation frequency per document. 107224 107224

Minimum in seq length: 0

Maximum list length: 20000000000

### Post Processing: Minimum Match (08

**Mexican**

Maximalist Mat (c) 1998  
 First Day First of Summer

Swissair AG: \*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMAB 11.5

Result	Score	Utility	Match	Length	DB	ID	Description
No.							
1	1161	100.0	530	1	ESR2_HUMAN	Q92731	homo sapiens
2	1161	99.9	279	1	ESR2_MOUSE	Q92731	mus musculus
3	1165	99.1	527	1	ESR2_SHEEP	Q92731	ovis montanus
4	1161	95.8	527	1	ESR2_PIG	Q92731	sus scrofa
5	1113	94.1	530	1	ESR2_PAT	Q92731	canis familiaris
6	1105	91.6	530	1	ESR2_MOUSE	Q92731	mus musculus
7	1103.5	91.4	526	1	ESR2_PIG	Q92731	sus scrofa
8	1103	91.4	530	1	ESR2_MOUSE	Q92731	mus musculus
9	1052	89.9	454	1	ESR2_PIG	Q92731	sus scrofa
10	1058	89.6	472	1	ESR2_PIG	Q92731	sus scrofa
11	1036	88.4	472	1	ESR2_PIG	Q92731	sus scrofa
12	842	70.4	610	1	ESR2_MOUSE	Q92731	mus musculus
13	840	70.4	573	1	ESR2_MOUSE	Q92731	mus musculus
14	835	69.7	575	1	ESR2_MOUSE	Q92731	mus musculus
15	820	69.4	568	1	ESR2_MOUSE	Q92731	mus musculus
16	820	69.4	568	1	ESR2_MOUSE	Q92731	mus musculus
17	809	68.5	559	1	ESR2_MOUSE	Q92731	mus musculus
18	787	67.5	557	1	ESR2_MOUSE	Q92731	mus musculus
19	765	67.2	474	1	ESR2_MOUSE	Q92731	mus musculus
20	741	67.0	565	1	ESR2_MOUSE	Q92731	mus musculus
21	711	65.3	589	1	ESR2_MOUSE	Q92731	mus musculus
22	709	65.0	587	1	ESR2_MOUSE	Q92731	mus musculus
23	709	64.3	595	1	ESR2_MOUSE	Q92731	mus musculus
24	706	64.0	599	1	ESR2_MOUSE	Q92731	mus musculus
25	703	63.8	595	1	ESR2_MOUSE	Q92731	mus musculus
26	700	63.5	600	1	ESR2_MOUSE	Q92731	mus musculus
27	709	63.4	595	1	ESR2_MOUSE	Q92731	mus musculus
28	745.5	63.4	525	1	ESR2_MOUSE	Q92731	mus musculus
29	705	62.5	585	1	ESR2_MOUSE	Q92731	mus musculus
30	705	62.2	549	1	ESR2_MOUSE	Q92731	mus musculus
31	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
32	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
33	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
34	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
35	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
36	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
37	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
38	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
39	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
40	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
41	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
42	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
43	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
44	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
45	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
46	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
47	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
48	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
49	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
50	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
51	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
52	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
53	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
54	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
55	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
56	704	62.2	565	1	ESR2_MOUSE	Q92731	mus musculus
57	704	62.2	565	1	ESR2_MOUSE	Q92731	mus

## ALIGNMENTS

**RESULT 1**

ID	ESR2_HUMAN	STANDARD	PRI	5' end AA
AC	C92741	606688	675584	607662
AC	G94946	G94946	675584	607662
DI	15-JUL-1999	(Ref. 48, 'treated')		
DI	15-JUL-1999	(Ref. 48, last sequence update)		
DI	16-OCT-2001	(Ref. 40, last annotation update)		
DE	Estragen receptor beta (ER-beta).			
GN	ESR2 OR NR3A2 OR ESRB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]	SEQUENCE FROM N.A. (ISOPFORM BETA-1).		
RP	MEDLINE:98139678; PubMed:947491;			
RA	Ogawa S., Inoue S., Watanabe T., Hiroi H., Urano A., Hosoi T.,			
RA	Ouchi Y., Muramatsu M.:			
R1	"The complete primary structure of human estrogen receptor beta			
R1	(hepbeta) and its heterodimerization with ER alpha in vivo and in			
R1	vitro."			
R1	Biochem. Biophys. Res. Commun. 241:122-126(1998).			
RN	[2]	SEQUENCE FROM R.A. AND ALTERNATIVE SPLICING.		
RC	Tissue Testis and Prostat:			
RC	MUTLINE:98359285; PubMed:94457;			
FA	Moore J.T., McKee D.D., Slonec Koster F., Moore L.R., Jones S.A.,			
FA	Harvie E.L., Su J., Lee Kleeber S.A., Jaymann J.M., Willson J.M.:			
RT	"Cloning and characterization of human estrogen receptor beta			
RT	isoforms."			
RL	Biochem. Biophys. Res. Commun. 247:75-78(1998).			
RL	[3]	SEQUENCE OF 425 bp FROM R.A. (15'-PDBE BETA-1), AND CHANATERRIATIN.		
RT	EST TESTIS AND PROSTAT:			
RT	MUTLINE:98359285; PubMed:8769413;			
EX	Moselman S., Polman J., DiKuma P.,			
EX	"Er beta: Identification and characterization of a novel human			
EX	estrogen receptor."			
RL	FEBS Lett. 392:149-151(1996).			
RL	[4]	SEQUENCE FROM R.A. (15'-PDBE BETA-2/CX), AND CHANATERRIATIN.		
RC	MUTLINE:98379282; PubMed:9671811;			
RC	Ogawa S., Inoue S., Watanabe T., Urano A., Hosoi T., Ouchi Y.,			
RA	Muramatsu M.:			
RA	"Molecular cloning and characterization of human estrogen receptor			
RA	beta cx: a potential inhibitor of estrogen action in human."			
RT	Nucleic Acids Res. 26:2595-2512(1998).			
RL	[5]	SEQUENCE OF 59-510 FROM N.A. (ISOPFORM BETA-5A AND BETA-6).		
RP	TISSUE Endometrium			
RC	Brandenberger A.W., Labovic D., Taylor R.N., Datta R.K.,			
RC	Schmidt C. (1998); from the PMID:9606047abstract abstracts.			
RI	[6]	SEQUENCE FROM R.A. (15'-PDBE BETA-2A).		
RN				



















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1b	FIG1B	ATP1A2	AACT1	1
1c	FIG1C	FIG1B	FIG1B	1
1d	FIG1D	FIG1B	FIG1B	1
1e	FIG1E	FIG1B	FIG1B	1
1f	FIG1F	FIG1B	FIG1B	1
1g	FIG1G	FIG1B	FIG1B	1
1h	FIG1H	FIG1B	FIG1B	1
1i	FIG1I	FIG1B	FIG1B	1
1j	FIG1J	FIG1B	FIG1B	1
1k	FIG1K	FIG1B	FIG1B	1
1l	FIG1L	FIG1B	FIG1B	1
1m	FIG1M	FIG1B	FIG1B	1
1n	FIG1N	FIG1B	FIG1B	1
1o	FIG1O	FIG1B	FIG1B	1
1p	FIG1P	FIG1B	FIG1B	1
1q	FIG1Q	FIG1B	FIG1B	1
1r	FIG1R	FIG1B	FIG1B	1
1s	FIG1S	FIG1B	FIG1B	1
1t	FIG1T	FIG1B	FIG1B	1
1u	FIG1U	FIG1B	FIG1B	1
1v	FIG1V	FIG1B	FIG1B	1
1w	FIG1W	FIG1B	FIG1B	1
1x	FIG1X	FIG1B	FIG1B	1
1y	FIG1Y	FIG1B	FIG1B	1
1z	FIG1Z	FIG1B	FIG1B	1

Country	Moldova	70, 44	Section	842	DB	1	Length	610	
Host	Local Ministry	70, 49	Prod. No.	9, 30	70				
Material	164	Conservation	44	Measurement	44	Endos	2	Gaps	2

14	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413
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1991, 1994  
1994, 1995

[illegible]









SEQUENCE FROM N.A.

ESTR4\_MITCN

BA HAWKINS M.B., THORNTON J.W., CROWDS D., SKIPPER J.K., DODD A., THOMAS P.J.

BA "Identification of a third distinct estrogen receptor and reclassification of estrogen receptors in teleosts."

BA Proc. Natl. Acad. Sci. U.S.A. 97:10751-10756(2000).

BA 1. FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF ER ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.

BA 2. SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER ALPHA (BY SIMILARITY).

BA 3. TISSUE SPECIFICITY: Abundant in the liver and testes, less abundant in the ovary and barely detectable in the muscle.

BA 4. DNA BINDING: FORMS A MODULATING TERTIARY COMPLEX WITH ER ALPHA AND ER BETA IN THE PRESENCE OF ESTROGEN.

BA 5. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

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BA 7. EMBL: AF298192; AAC16712.1.

BA 8. InterPro: IP000546; Hormone\_rec\_119.

BA 9. InterPro: IP000441; Steroid\_h.

BA 10. InterPro: IP001728; Steroid\_hormone\_rec\_119.

BA 11. InterPro: IP001628; Z1\_C4.

BA 12. Pfam: PF00104; Hormone\_rec\_1.

BA 13. Pfam: PF00104; Korf\_1.

BA 14. PRINTS: PR00198; STRD0060606.

BA 15. PRINTS: PR00047; STRD0010606.

BA 16. SMART: SM00403; HOLL\_1.

BA 17. SMART: SM00403; Z0E\_C4\_1.

BA 18. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 19. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 20. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 21. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 22. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 23. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 24. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 25. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 26. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 27. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 28. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 29. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 30. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 31. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 32. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 33. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 34. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

RESULT 20

ESTR4\_MITCN

BA HAWKINS M.B., THORNTON J.W., CROWDS D., SKIPPER J.K., DODD A., THOMAS P.J.

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BA 7. EMBL: AF298192; AAC16712.1.

BA 8. InterPro: IP000546; Hormone\_rec\_119.

BA 9. InterPro: IP000441; Steroid\_h.

BA 10. InterPro: IP001728; Steroid\_hormone\_rec\_119.

BA 11. InterPro: IP001628; Z1\_C4.

BA 12. Pfam: PF00104; Hormone\_rec\_1.

BA 13. Pfam: PF00104; Korf\_1.

BA 14. PRINTS: PR00198; STRD0060606.

BA 15. PRINTS: PR00047; STRD0010606.

BA 16. SMART: SM00403; HOLL\_1.

BA 17. SMART: SM00403; Z0E\_C4\_1.

BA 18. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 19. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 20. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 21. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 22. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 23. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 24. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 25. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 26. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 27. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 28. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 29. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 30. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 31. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 32. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 33. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

BA 34. PROSITE: PS00031; NUCLEAR\_BINDING\_1.

[illegible]

DR	SWARTZ: S8004-00; ROL1; 1.
DR	SMAPI; P8009; ZNF-74; 1.
DR	PROSTTE; P80041; NUCLEAR-RECEPTOR; 1.
KW	Receptor; Transcription regulation; RNA binding; Nuclear protein;
KW	Zinc-finger; Steroid-binding.
FT	366716; 129
FT	UNAFIND; 179; 244; M-FOLD-TRIP;
FT	ZNF1160; 179; 159; NUCLEAR RECEPTOR-TYPE;
FT	ZNFJING; 215; 239; C4-TYPE;
FT	ZNFJING; 215; 239; C4-TYPE;
FT	ZNFJING; 215; 239; HINCE;
FT	DOMAIN; 305; 589; STEROID-BINDING;
FT	SPRING; 59; 64; 306; TROV-270A5AB GRCv4.1
Query Match	65.48; Score 771; 1061; Length 589;
Best Local Similarity	62.1%; Pred. No. 4,24-64;
Matches 14;	Coverage 100; Missed 41; Indels 2; Gaps 27
DY	1 FATHLEHHHLLLS-PGSAETFASSMMSLTATPFLVGMISKKKQCHLSEPT; 59
DB	309 MSNALLPAEPPLVYSSTVDNPPEASMSMLTLINAIPELVIMAKKRVGVITLTD; 608
DY	60 QVRILSSWMVEVMMLMKSITHMKLFAPRVLVLDDEKQVENIIFTHMLATSR; 119
DB	359 GVHLIEVAMEHLMGLVWEHMHCFLIAIRLLDENGKEVDMVTTPMLIAAR; 428
DY	120 PRRLTGHTLYELVKAMILLNSMTIVLAIGDALSGSLAH-LIANVAIVAVIAS; 178
DB	429 EPMONTGPEPTVTKSIIHSNVLISSIKSKPRGYHVEVCSTDTLRMAKSS; 488
DY	179 LFGVGGMEFANLWTAEVGSAPTMHIGPSFAYVVVVFPPFNAVF; 234
DB	489 LSYGHEPLACELLTSHEMSAPGRHYNNCPENVAVVQLLPMLIAAR; 548
RESULT 22	
ID	ESR1_PORCU
ID	ESR1_PORCEN
AC	091250;
UT	15-JUL-1999 (Ref. 38, Created)
DT	15-JUL-1999 (Ref. 38, Last sequence update)
DI	15-JUL-1999 (Ref. 38, Last annotation update)
DE	Histrogen receptor (hsr) (histadiol receptor) (hr-alpha).
GN	ESR1 OR NR3A1 OR ESR.
OS	Popillia guttata (Zeppia linch) (Taenioptila guttata);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Atherinaria; Aves; Neornithae; Passeriformes; Estrildidae;
OC	Facioliinae; Taenioptila;
OX	NCHI_TaxID=59729;
RN	[1]
RP	SEQUENCE FROM N.A.
RT	TISSUE-HYPOTHALAMUS;
RX	MEDLINE: 97163508; PubMed: 9010328;
RA	JACOBS E.C.; ARNOID A.P.; CAMPBELL A.L.;
TA	"Zeppia linch" estrogen receptor cDNA: cloning and mRNA expression.";
RI	J. Steroid Biochem. Mol. Biol. 59:135-145(1999);
CC	-1 FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC	1st SECRETATION; 2nd FACULTATIVE GENE EXPRESSION AND ADAPT CELLULAR
CC	PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC	-1 SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER
CC	BETA (BY SIMILARITY).
CC	-1 SUBCELLULAR LOCATION: Nuclear.
CC	-1 DOMAIN: COMPOSED OF THREE DOMAINS. A MEDIATING N-TERMINAL DOMAIN,
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC	-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC	NR3 SUPERFAMILY.
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
CC	at the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
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117) X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 182-262.  
 118) MEDLINE 9402710; PUBMED 822195;  
 119) Schwabe J.W.E., Chapman L., Fitch J.T., Rhodes D.  
 120) "The crystal structure of the estrogen receptor DNA-binding domain  
 121) bound to DNA: how receptors discriminate between their response  
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 123) CELL 75:567-578(1993).  
 124) X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.  
 125) MEDLINE 9747859; PUBMED 918790;  
 126) DODOWSKI A.W., EIKS A.C.W., FRYER J., HUBARD P.E., BEN T.  
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 128) "Molecular basis of agonism and antagonism in the estrogen  
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 131) X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 306-544.  
 132) MEDLINE 98261297; PUBMED 960906;  
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 135) receptors' ligand binding domains".  
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 137) X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 294-554.  
 138) MEDLINE 99091051; PUBMED 9875847;  
 139) SETHI A.K., GREENE G.L., LORIA P.W., Cheng T., Kushner P.J.,  
 140) "The structural basis of estrogen receptor/coactivator recognition  
 141) and the antagonism of this interaction by tamoxifen".  
 142) CELL 95:927-937(1998).  
 143) 4D-STRUCTURE MODELING OF 311-547.  
 144) MEDLINE 98280606; PUBMED 943697;  
 145) Maudslott G.L., Xu W., Smith T., Mohr S.C.  
 146) "Molecular model for the ligand binding domain of the human estrogen  
 147) receptor".  
 148) J. Biol. Struct. Dyn. 15:841-850(1998).  
 149) VARIANT VAL-400.  
 150) MEDLINE 9729712; PUBMED 937792.  
 151) Tada E., Mullick A., Bretzner D., Fendliklimoguel M., Park I.,  
 152) Champion P.  
 153) "The cloned human estrogen receptor contains a mutation which alters  
 154) its hormone binding properties".  
 155) EMBO J. 8:1981-1986(1989).  
 156) VARIANT ALA-447.  
 157) MEDLINE 9729712; PUBMED 937792.  
 158) Rose J.C., Katzenellenbogen B.S.  
 159) "Characterization of a temperature-sensitive mutation in the hormone  
 160) binding domain of the human estrogen receptor. Studies in the hormone  
 161) extracts and intact cells and their implications for  
 162) hormone-dependent transcriptional activation".  
 163) J. Biol. Chem. 267:9868-9873(1992).  
 164) VARIANT GLU-464.  
 165) MEDLINE 9712959; PUBMED 8961252;  
 166) McIntire B.M., Ince B.A., Shapiro D., Katzenellenbogen B.S.  
 167) "A temperature-sensitive mutation in the DNA binding domain of the  
 168) of dominant negative inhibitor of estrogen action".  
 169) Mol. Endocrinol. 10:1519-1526(1996).  
 170) VARIANT CYS-160.  
 171) MEDLINE 9738862; PUBMED 9405937;  
 172) Johnson T.E., Wawter E., Lippa K., Collins R., Warren M., Shabo M.,  
 173) Estler F., Tavit K.M., Johnson S.D., Fowles M., Olsen A.O.  
 174) "Screening for RSP mutations in breast and ovarian cancer patients".  
 175) Hum. Mutat. 9:541-543(1997).  
 176) -1- PURIFICATION OF ESTROGEN HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 177) PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

```
CC      1 SUBUNIT_1 BINDS DNA AS A HORMONEMIMIC. CAN FORM A DIMER WITH ER-
CC      BETA.
CC      -1 SUBCELLULAR LOCATION: Nuclear.
CC      -1 ALTERNATIVE PROPERTIES: AT LEAST TWO FORMS ARE PRODUCED BY
CC      ALTERNATIVE SPLICING.
CC      -1 DOMAIN COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC      A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC      1 ELM_HOMOLOGOUSLY BY CYCLIN AZIDE. PHOSPHORYLATION PROBABLY
CC      ENHANCES TRANSCRIPTIONAL ACTIVITY.
CC      -1 MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS
CC      ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;
CC      IFERONE BINDING GREATLY INCREASES RECEPTOR ACTIVITY. THE
CC      -1 BEFORE EFFECT OF GMPFF AFFAIRS TO PREVENT THE EXPRESSION OF RNA
CC      SEQUENCES BETWEEN OF TRANSCRIPTIONAL START SITES.
CC      -1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC      NR3 SUPERFAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed, used by and for commercial
CC      entities requires a license agreement (see http://www.isdb.ch).
CC      or send an email to license@isdb.ch.
CC      CC
CC      EMBL: X03635; CAA27284.1; -.
CC      FNU: M16671; AAA62399.1; -.
CC      DR   EMBL: U47678; AA000115.1; -.
CC      DR   EMBL: X73057; CAA51528.1; -.
CC      DR   EMBL: AF123503; AAC52984.1; -.
CC      DR   EMBL: AF123494; AAC52984.1; JOINED.
CC      -----
Query Match          64.3% Score 759; DB 1; Length 595;
Post local similarity 60.2%; Prog No 5 50-63;
Matches 142; Conservative 54; Mismatches 36; Indels 4; Gaps 3;
CC      CC
CY      1 LVLTLEAPPIHLISK--PSAFTFAASMMMSITLAKEIVIMISNAKKIPGVLSLP 58
DB      315 MSVALDADEP ILSVDFTEFSASMDLLTMADRLVIMISNAKVPQGVDTTH 373
CC      EV TAVVTLLEAMVAVNLTWVFLEGLGDLAFGLVLRSGKVTFETFGAGATTA 118
CC      II III III III III III III III III III III III III III III
DB      374 DVHILLECALFLMIGLVWSRHEHGKLLFPNILLDPNSKVPQGVDTPLATSS 433
CC      OY      119 PPEELIKGRREVLCVAMLLINSMTVEVTAI-QVAISSKIAHLINAVITAAVWVAES 177
CC      FB      434 PFPMRILOCHNVSKELLINSOVTVTSSTLKSLSEKPK;EPVILPTTRV IGMAPA 493
CC      ZJ      378 GTSQQSQEQEAVLMLCTSVPLASRKREVELLNRCGVAVVGHIIIPYNAIVE 244
CC      DB      494 GLTIQDDHRLALLLIISHIRMSKKOHILYSKCKRVVPLTDLLIMIAHKL 549
CC      -----
RESULT 24
ID      ESRL MOUSE STANDARD: PRI: 599 AA.
AC      PI9785; Q9GY51; Q9GY52;
DC      01-FEB-1991 (Ref. 17, Created)
PC      01-FEB-1991 (Ref. 17, Last sequence update)
SF      01-FEB-1991 (Ref. 11, Last annotation update)
DE      Estradiol receptor (ER), estradiol receptor (ER-alpha).
GN      ESRL OR NP3A1 OR ESP OR ESTP OR ESTRA.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC      FNMI1a1b-10000;
CX      (1)
RN      SEQUENCE FROM N.A.
PG      TISSUE-Oterus;
EX      MEDLINE:91042558; PubMed:2484714;
NA      White R., Lees J.A., Needham M., Han J., Parker M.;
RT      "Structural organization and expression of the mouse estrogen
BT      receptor.";
```

[illegible]











Journal Pre-proof

Journal Pre-proof

100

























GenCore version 4.5  
Copyright (c) 1994 - 2000 CompuGen Ltd.

[illegible]

Table 1	July 12, 2002, 14:55:47 : Search time 19.93 Seconds (without alignments)
161.448 Million cell updates/sec	

10012001	886
10012002	10012003

[illegible]

105,224 seqs, 3871,950 residues

total number of hits satisfying chosen parameters: 105224

2000000000

[illegible][illegible]

Proof.  $N_i$  is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SİMMAKİS

No.	S.	Gen.	Locality	Alt.	Specimen
1	486	100.0	472	1	ESR2, CHIK
2	486	100.0	472	1	ESR2, CHIK
3	386	100.0	526	1	ESR2, PIG
4	386	100.0	527	1	ESR2, BEVIN
5	386	100.0	527	1	ESR2, SHEEP
6	386	100.0	530	1	ESR2, CALIA
7	386	100.0	530	1	ESR2, HORAN
8	386	100.0	540	1	ESR2, MOUSE
9	386	100.0	554	1	ESR2, STYVA
10	386	100.0	568	1	ESR1, CARAU
11	386	100.0	568	1	ESR2, ORNOV
12	386	100.0	568	1	ESR2, VITAN
13	386	100.0	568	1	ESR2, VITAN
14	386	100.0	566	1	ESR1, XINIA
15	386	100.0	569	1	ESR1, MOARE
16	386	100.0	530	1	ESR1, RAI
17	386	100.0	557	1	ESR2, VITAN
18	386	100.0	527	1	ESR2, CHIK
19	386	100.0	527	1	ESR2, CHIK
20	386	100.0	527	1	ESR2, CHIK
21	386	100.0	527	1	ESR2, CHIK
22	386	100.0	527	1	ESR2, CHIK
23	386	100.0	527	1	ESR2, CHIK
24	386	100.0	527	1	ESR2, CHIK
25	386	100.0	527	1	ESR2, CHIK
26	386	100.0	527	1	ESR2, CHIK
27	386	100.0	527	1	ESR2, CHIK
28	386	100.0	527	1	ESR2, CHIK
29	386	100.0	527	1	ESR2, CHIK
30	386	100.0	527	1	ESR2, CHIK
31	386	100.0	527	1	ESR2, CHIK
32	386	100.0	527	1	ESR2, CHIK
33	386	100.0	527	1	ESR2, CHIK
34	386	100.0	527	1	ESR2, CHIK
35	386	100.0	527	1	ESR2, CHIK
36	386	100.0	527	1	ESR2, CHIK
37	386	100.0	527	1	ESR2, CHIK
38	386	100.0	527	1	ESR2, CHIK
39	386	100.0	527	1	ESR2, CHIK
40	386	100.0	527	1	ESR2, CHIK
41	386	100.0	527	1	ESR2, CHIK
42	386	100.0	527	1	ESR2, CHIK
43	386	100.0	527	1	ESR2, CHIK
44	386	100.0	527	1	ESR2, CHIK
45	386	100.0	527	1	ESR2, CHIK
46	386	100.0	527	1	ESR2, CHIK
47	386	100.0	527	1	ESR2, CHIK
48	386	100.0	527	1	ESR2, CHIK
49	386	100.0	527	1	ESR2, CHIK
50	386	100.0	527	1	ESR2, CHIK
51	386	100.0	527	1	ESR2, CHIK
52	386	100.0	527	1	ESR2, CHIK
53	386	100.0	527	1	ESR2, CHIK
54	386	100.0	527	1	ESR2, CHIK
55	386	100.0	527	1	ESR2, CHIK
56	386	100.0	527	1	ESR2, CHIK
57	386	100.0	527	1	ESR2, CHIK
58	386	100.0	527	1	ESR2, CHIK
59	386	100.0	527	1	ESR2, CHIK
60	386	100.0	527	1	ESR2, CHIK
61	386	100.0	527	1	ESR2, CHIK
62	386	100.0	527	1	ESR2, CHIK
63	386	100.0	527	1	ESR2, CHIK
64	386	100.0	527	1	ESR2, CHIK

[illegible]

Run	Monomer	Feed	Conv.	$\bar{M}_n$	$\bar{M}_w$	$\bar{M}_w/\bar{M}_n$	$\bar{M}_n$	$\bar{M}_w$	$\bar{M}_w/\bar{M}_n$
1	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
2	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
3	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
4	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
5	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
6	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
7	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
8	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
9	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
10	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
11	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
12	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
13	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
14	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
15	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
16	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
17	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
18	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
19	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
20	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
21	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
22	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
23	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
24	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
25	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
26	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
27	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
28	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
29	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
30	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
31	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
32	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
33	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
34	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
35	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
36	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5
37	MA	0.5	0.95	10,000	15,000	1.5	10,000	15,000	1.5

Energy Match:	100.0%;	Storage: 000; DB: 1;	Length: 42;
Local Simulation:	100.0%;	Prod. No.: 20;	45;
Match:	45;	Minimization:	0;
		Index:	0;
		Case:	0;

[illegible]

PERIOD 2	STANDARD	1.85%	47.2 AA
PERIOD 1	STANDARD	1.85%	47.2 AA

**TABLE 6**

(d)	Booth's 2001 (Boat, 40), last update)
(e)	Booth's 2001 (Boat, 40), last sequence update)
(f)	Booth's 2001 (Boat, 40), last arrival time update)
(g)	Eulerian tour problem (Euler boat).

END OF NFA.

190. Pink eye (conj. Mollusc); Choroid; Trachoma; Verticillate; Enterozoostomy.  
 191. Alveolar fat; Aorta; Nephrotic body; Endothelium; Mesothelium; Phosphatase  
 192. Conduits.  
 193. Nephrotic body.

PA. Ronald A., Lukoye, B., Girard, T., Hall, G.F., Balchowitz, J., et al. "Sequence and nonrandom distribution of estrogen receptor in the adult brain."

IP	3110100N°E, 44° 14' 28.6, 17° 00' N, A
LO	133500E, 108° 13'
EX	MULTI-ENERGY SURVEY, 1700Mcd, 07260

PL. *arizonae* Knuth,"  
 EL. *Monograph* 9, 274 (1908).  
 OF. 1. *PERITOMIA*. *HERBES* DIVERSES. *WILLIAM* AND *AUTHORITY* *PROPOSAL* *IN* "WHAT OF

1. SCHUBERT, HENRI, et al. A. A. 23. 1955. *CA*. 1: 444. A. 1911. 1912. 1913. 1914. 1915. 1916. 1917. 1918. 1919. 1920. 1921. 1922. 1923. 1924. 1925. 1926. 1927. 1928. 1929. 1930. 1931. 1932. 1933. 1934. 1935. 1936. 1937. 1938. 1939. 1940. 1941. 1942. 1943. 1944. 1945. 1946. 1947. 1948. 1949. 1950. 1951. 1952. 1953. 1954. 1955. 1956. 1957. 1958. 1959. 1960. 1961. 1962. 1963. 1964. 1965. 1966. 1967. 1968. 1969. 1970. 1971. 1972. 1973. 1974. 1975. 1976. 1977. 1978. 1979. 1980. 1981. 1982. 1983. 1984. 1985. 1986. 1987. 1988. 1989. 1990. 1991. 1992. 1993. 1994. 1995. 1996. 1997. 1998. 1999. 2000. 2001. 2002. 2003. 2004. 2005. 2006. 2007. 2008. 2009. 2010. 2011. 2012. 2013. 2014. 2015. 2016. 2017. 2018. 2019. 2020. 2021. 2022. 2023. 2024. 2025. 2026. 2027. 2028. 2029. 2030. 2031. 2032. 2033. 2034. 2035. 2036. 2037. 2038. 2039. 2040. 2041. 2042. 2043. 2044. 2045. 2046. 2047. 2048. 2049. 2050. 2051. 2052. 2053. 2054. 2055. 2056. 2057. 2058. 2059. 2060. 2061. 2062. 2063. 2064. 2065. 2066. 2067. 2068. 2069. 2070. 2071. 2072. 2073. 2074. 2075. 2076. 2077. 2078. 2079. 2080. 2081. 2082. 2083. 2084. 2085. 2086. 2087. 2088. 2089. 2090. 2091. 2092. 2093. 2094. 2095. 2096. 2097. 2098. 2099. 2100. 2101. 2102. 2103. 2104. 2105. 2106. 2107. 2108. 2109. 2110. 2111. 2112. 2113. 2114. 2115. 2116. 2117. 2118. 2119. 2120. 2121. 2122. 2123. 2124. 2125. 2126. 2127. 2128. 2129. 2130. 2131. 2132. 2133. 2134. 2135. 2136. 2137. 2138. 2139. 2140. 2141. 2142. 2143. 2144. 2145. 2146. 2147. 2148. 2149. 2150. 2151. 2152. 2153. 2154. 2155. 2156. 2157. 2158. 2159. 2160. 2161. 2162. 2163. 2164. 2165. 2166. 2167. 2168. 2169. 2170. 2171. 2172. 2173. 2174. 2175. 2176. 2177. 2178. 2179. 2180. 2181. 2182. 2183. 2184. 2185. 2186. 2187. 2188. 2189. 2190. 2191. 2192. 2193. 2194. 2195. 2196. 2197. 2198. 2199. 2200. 2201. 2202. 2203. 2204. 2205. 2206. 2207. 2208. 2209. 2210. 2211. 2212. 2213. 2214. 2215. 2216. 2217. 2218. 2219. 2220. 2221. 2222. 2223. 2224. 2225. 2226. 2227. 2228. 2229. 2230. 2231. 2232. 2233. 2234. 2235. 2236. 2237. 2238. 2239. 2240. 2241. 2242. 2243. 2244. 2245. 2246. 2247. 2248. 2249. 2250. 2251. 2252. 2253. 2254. 2255. 2256. 2257. 2258. 2259. 2260. 2261. 2262. 2263. 2264. 2265. 2266. 2267. 2268. 2269. 2270. 2271. 2272. 2273. 2274. 2275. 2276. 2277. 2278. 2279. 2280. 2281. 2282. 2283. 2284. 2285. 2286. 2287. 2288. 2289. 2290. 2291. 2292. 2293. 2294. 2295. 2296. 2297. 2298. 2299. 2300. 2301. 2302. 2303. 2304. 2305. 2306. 2307. 2308. 2309. 2310. 2311. 2312. 2313. 2314. 2315. 2316. 2317. 2318. 2319. 2320. 2321. 2322. 2323. 2324. 2325. 2326. 2327. 2328. 2329. 2330. 2331. 2332. 2333. 2334. 2335. 2336. 2337. 2338. 2339. 2340. 2341. 2342. 2343. 2344. 2345. 2346. 2347. 2348. 2349. 2350. 2351. 2352. 2353. 2354. 2355. 2356. 2357. 2358. 2359. 2360. 2361. 2362. 2363. 2364. 2365. 2366. 2367. 2368. 2369. 2370. 2371. 2372. 2373. 2374. 2375. 2376. 2377. 2378. 2379. 2380. 2381. 2382. 2383. 2384. 2385. 2386. 2387. 2388. 2389. 2390. 2391. 2392. 2393. 2394. 2395. 2396. 2397. 2398. 2399. 2400. 2401. 2402. 2403. 2404. 2405. 2406. 2407. 2408. 2409. 2410. 2411. 2412. 2413. 2414. 2415. 2416. 2417. 2418. 2419. 2420. 2421. 2422. 2423. 2424. 2425. 2426. 2427. 2428. 2429. 2430. 2431. 2432. 2433. 2434. 2435. 2436. 2437. 2438. 2439. 2440. 2441. 2442. 2443. 2444. 2445. 2446. 2447. 2448. 2449. 2450. 2451. 2452. 2453. 2454. 2455. 2456. 2457. 2458. 2459. 2460. 2461. 2462. 2463. 2464. 2465. 2466. 2467. 2468. 2469. 2470. 2471. 2472. 2473. 2474. 2475. 2476. 2477. 2478. 2479. 2480. 2481. 2482. 2483. 2484. 2485. 2486. 2487. 2488. 2489. 2490. 2491. 2492. 2493. 2494. 2495. 2496. 2497. 2498. 2499. 2500. 2501. 2502. 2503. 2504. 2505. 2506. 2507. 2508. 2509. 2510. 2511. 2512. 2513. 2514. 2515. 2516. 2517. 2518. 2519. 2520. 2521. 2522. 2523. 2524. 2525. 2526. 2527. 2528. 2529. 2530. 2531. 2532. 2533. 2534. 2535. 2536. 2537. 2538. 2539. 2540. 2541. 2542. 2543. 2544. 2545. 2546. 2547. 2548. 2549. 2550. 2551. 2552. 2553. 2554. 2555. 2556. 2557. 2558. 2559. 2560. 2561. 2562. 2563. 2564. 2565. 2566. 2567. 2568. 2569. 2570. 2571. 2572. 2573. 2574. 2575. 2576. 2577. 2578. 2579. 2580. 2581. 2582. 2583. 2584. 2585.

AND ADRIAN, GLAND,  
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108	108597	108597.2	108597.1
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180	108669	108669.1	108669.0

PRIN1S; PRIN047; SKELETONIZER  
SMO1; SMO44; and 1

**KW** Zinc finger; Steroid-binding.  
**RE** ZINC FINGER; STEROID-BINDING.

Sample	Stoichiometry	AA	MM	Defect Density (10 <sup>18</sup> cm <sup>-3</sup> )
P1	2Zn:1Fe	1.71	1.22	4.4
P2	2Zn:1Fe	1.41	1.65	5.4
P3	10Fe:1Mn	1.71	4.72	5.4
S0	Stoichiometric	4.72	5.41	1.7

Query Match	100, 0%; Score 486; DR 1; Length 472
Host Local Similarity	100, 0%; Prod. No. 20-45;
Matches	66; Mismatches 0; Indels

[illegible]

11.  $\frac{1}{2} \sqrt{2}$       12.  $\frac{1}{2} \sqrt{2}$       13.  $\frac{1}{2} \sqrt{2}$       14.  $\frac{1}{2} \sqrt{2}$       15.  $\frac{1}{2} \sqrt{2}$

LD	ESR2 P10	STANFORD	PRT	526 AA
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 RN 11  
 SOLUTION: FROM N. A.  
 001 FLSH: 10ml vial

12. "Methodical handling of post-operative recipient beta cells derived from fetal pancreas in post-transplantation diabetes." *Endocrinology* 1996;138:1001-1006.

RA  
LaVoie H.A., Ioshimaru J.,  
1991, and expression of estrogen receptor beta isoforms from

1. **PERSONS ENTERING WITH AN AFFINITY SIMILAR TO THAT OF**  
**THE AFFINITY AND A FAVORABLE EXPRESSION OF THEIR OPINIONS CONTAINING**  
**INFORMATION CONCERNING THE AFFINITY IN AN EXTENSIVE DETERMINED MANNER**

**07-1** SUBCELLULAR LOCALIZATION: Nucleolus.  
**07-2** FUNCTIONAL CLASSIFICATION: A MAINTAINING & ESTABLISHING CHROMATIN DOMAIN. A MEMBER OF THREE DOMAINS: A MAINTAINING CHROMATIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

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ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.  
 1. SUBUNIT: HINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-  
 ALPHA (BY SIMILARITY).  
 1. SUBCELLULAR LOCATION: Nucleolus.  
 1. DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.  
 1. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 NRY SUBFAMILY.

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 OR SEND AN EMAIL TO [license@isb.slb.ch](mailto:license@isb.slb.ch)).

EMBL: U75607; AN000246.1;  
 HENR5: P04472; IBCP;  
 InterPro: IPR000546; Hormone\_rec\_10;  
 InterPro: IPR017243; Steroidhormone\_receptor;  
 InterPro: IPR016286; Z1-C4;  
 Pfam: PF00104; Hormone\_rec\_1;  
 Pfam: PF00105; Z1-C4; 1;  
 PRINTS: PR00098; STEROIDHORMONER;  
 PRINTS: PR00047; STEROIDRECEPTOR;  
 SMART: SM00409; HOLL1; 1;  
 SMART: SM00409; ZNF\_C4; 1;  
 PROSITE: PS00043; NUCLEAR\_RECEPTOR; 1;  
 Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 Zinc finger; Steroid binding;  
 Domain  
 1 154 MODULATING;  
 E1 DNA BINDING 155 226 NUCLEAR RECEPTOR TYPE;  
 E1 ZN FING 155 175 C4-TYPE;  
 E1 ZN FING 191 215 C4-TYPE;  
 E1 DOMAIN 227 557 STEROID BINDING;  
 Sequence: 557 AA; 61779 MW; R2A47498690006; GPGC64;

\*Identification of a third distinct estrogen receptor and  
 reclassification of estrogen receptors in teleosts.\*;  
 RI Proc. Natl. Acad. Sci. U.S.A. 97:10751-10756(2000).  
 1. FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF  
 ER ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING  
 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.  
 1. SUBUNIT: HINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER  
 ALPHA (BY SIMILARITY).  
 1. SUBCELLULAR LOCATION: Nucleolus.  
 1. TISSUE SPECIFICITY: ABUNDANT IN THE LIVER AND TESTES, LESS  
 ABUNDANT IN THE OVARY AND BARELY DETECTABLE IN THE MUSCLE.  
 1. DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.  
 1. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 RNY SUBFAMILY.

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EMBL: AF298184; AN016711.1;  
 InterPro: IPR000546; Hormone\_rec\_10;  
 InterPro: IPR004641; Keratin;  
 InterPro: IPR017243; Steroidhormone\_receptor;  
 InterPro: IPR016286; Z1-C4;  
 Pfam: PF00104; Hormone\_rec\_1;  
 Pfam: PF02422; Keratin; 1;  
 PRINTS: PR00098; STEROIDHORMONER;  
 PRINTS: PR00047; STEROIDRECEPTOR;  
 SMART: SM00409; HOLL1; 1;  
 SMART: SM00409; ZNF\_C4; 1;  
 PROSITE: PS00043; NUCLEAR\_RECEPTOR; 1;









01 NUCLEOTIDE SEQUENCE OF 311-547.  
 02 PUBMED:98280806; PubMed 9815597.  
 03 MAJUMDAR S, XIA W, Smith T, Behr S.  
 04 "Functionally model for the ligand binding domain of the human estrogen  
 05 receptor".  
 06 J. Biol. Struct. Dyn. 15:841-850(1998).  
 07 [181]  
 08 VARIANT VAL-400.  
 09 PROTEIN: 98252593; PubMed 9730979.  
 10 LEE J, MILLER A, McArthur D, Frohlich-Greub M, Park T,  
 11 Chabon P.  
 12 "The cloned human estrogen receptor contains a mutation which alters  
 13 its hormone binding properties.".  
 14 EMBO J. 8:1981-1986(1989).  
 15 [19]  
 16 VARIANT ALA-447.  
 17 MAJUMDAR S, XIA W, Smith T, Behr S.  
 18 ROSE J.C., KATZMELLENBOMEN B.S.  
 19 "Characterization of a temperature-sensitive mutation in the hormone  
 20 binding domain of the human estrogen receptor. Studies in cell  
 21 extracts and intact cells and their implications for  
 22 hormone-dependent transcriptional activation".  
 23 J. Biol. Chem. 267:9868-9873(1992).  
 24 [20]  
 25 VARIANT GLN-464.  
 26 MAJUMDAR S, XIA W, Smith T, Behr S.  
 27 "Screening for ESR mutations in breast and ovarian cancer patients.".  
 28 A transcriptionally active estrogen receptor mutant is a novel type  
 29 of dominant negative inhibitor of estrogen action".  
 30 Mol. Endocrinol. 10:1519-1526(1996).  
 31 [21]  
 32 VARIANT CYS-160.  
 33 MAJUMDAR S, XIA W, Smith T, Behr S.  
 34 ANDERSON T.L., WOOTER P., HARRIS R., LITTON K., STRICK M.,  
 35 PAULSEN O., TROTT K.M., THOMPSON S.R., POWERS M., GIBSON A.C.,  
 36 MILLER P., STRATTON M.R., KOTROUS-DALE A.L.  
 37 "Screening for ESR mutations in breast and ovarian cancer patients.".  
 38 Hum. Mutat. 9:531-536(1997).  
 39 [22]  
 40 FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN  
 41 THE REGULATION OF ENDOCRINE GENE EXPRESSION AND ADAPT CHILUJAR  
 42 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.  
 43 [23]  
 44 SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-  
 45 BETA.  
 46 [24]  
 47 SUBCELLULAR LOCATION: Nucleus.  
 48 [25]  
 49 ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED BY  
 50 ALTERNATIVE SPLICING.  
 51 [26]  
 52 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 53 A DNA-BINDING DOMAIN, AND A C-TERMINAL STEROID BINDING DOMAIN.  
 54 [27]  
 55 PTM: PHOSPHORYLATED BY CYCLIN A27K2. HYDROXYLATION REGULARLY  
 56 ENHANCES TRANSCRIPTIONAL ACTIVITY.  
 57 [28]  
 59 MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS  
 60 ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;  
 61 HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE  
 62 HORMONE RECEPTOR COMPLEX APPEARS TO RECOGNIZE FISCHLE DNA  
 63 SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.  
 64 [29]  
 65 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 66 NPK SUPERFAMILY.  
 67 [30]  
 68 [31]  
 69 [32]  
 70 [33]  
 71 [34]  
 72 [35]  
 73 [36]  
 74 [37]  
 75 [38]  
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 77 [40]  
 78 [41]  
 79 [42]  
 80 [43]  
 81 [44]  
 82 [45]  
 83 [46]  
 84 [47]  
 85 [48]  
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 87 [50]  
 88 [51]  
 89 [52]  
 90 [53]  
 91 [54]  
 92 [55]  
 93 [56]  
 94 [57]  
 95 [58]  
 96 [59]  
 97 [60]  
 98 [61]  
 99 [62]  
 100 [63]

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Query Match Similarity      98.4% Score 360; DB L: Length 595;
Burst Local similarity     97.0%; Pred No.: 13e-44;
Matches    44,   Conserved          2, Missed       0,   Totals        0 - gaps
                                |
07              61 CEEVGM 66
                   |||||
DB             245 CEEVGM 250
                                |
RESULT 25
ESRL_MESAU                                     PRT:         595 AA.
ID ESRL_MESAU                               STANDARD:
AC GYGCJZ, GYGCSG:
PE 16 OCT 2001 (Rel. 40, Created)
PF 16-OCT-2001 (Rel. 40, last sequence update)
FT 16-OCT-2001 (Rel. 40, last annotation update)
FE Estrogen receptor (ER) (Estrogenic receptor) (R-alpha).
GN ESR1 OR NR3A1 OR ESR
OS Mesocricetus auratus (Golden hamster),
EN Enkaryota: Metazoa: Chordata: Gracilata: Vertebrata: Euarchontia:
MA Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Citellinae:
OC Mesocricetini.
OX NCBI_Taxid=10036;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE GENUS:
RX MEDLINE=20197937; PubMed 10731637;
RA Bhat H.K., Vadamana J.V.;
RT "hamster estrogen receptor cDNA, cloning and mRNA expression.";
EI 1 Steroid Biochem Mol Biol 72:47-53(2000);
FN [2]
PP SOURCE OF 98-291 FROM N.A.
RA Jones J.R., Carpenter C.D., Lukacs I.S., Peterson S.L., Wade G.N.;
RT "Return of lizards after food deprivation and refeeding in Syrian
hamsters."
PL Submitted (SEP-1995) to the FMR database databases.
CC -I FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
THE REGULATION OF ENKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CG -I SIROINTE RINDS RNA AS A HOMODIMER CAN FORM A HETERODIMER WITH ER-
BEFA (BY SIMILARITY).
CC -I SUBCELLULAR LOCATION: Nuclear.
CC -I DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA BINDING DOMAIN AND A C TERMINAL STEROID BINDING DOMAIN.
CZ 1 SIMILARITY: BELONGS TO THE NOCTURNAL HORMONE RECEPTORS FAMILY.
CN NS3 SUBFAMILY.
-----
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CC -----
OK EMBL, AF181077, AAC53956..1 ..
DR EMBL, AF184276, AAC02721..1 ;
DR HSDB, P03372; HQCP.
DP InterPro: IPFO00536; Hormone_rec_1lg.
PF Int-Fit: IFPO01292; Oest_recep.
InterPro: IPFO01293; Slrdomomre_receptor.
DP InterPro: IPFO01628; zf-C4.
PF Pfam: pf00104; hormone_recf_1.
DR Pfam: PF02159; Oest_recept_1.
PI Pfam: PF00105; zf_C4; 1.
PR PRINTS: PR00349; STRDOMOMRE.
DP PRINTS: PP00047; STROIDFINGER.
DP SMART: SM00440; HOL1; 1.
DP SMART: SM00399; Znf_C4; 1.
```







1 SUBCELLULAR LOCATION: Nucleus.  
 2 DOMAIN: COMPOSED OF THREE DOMAINS: A REGULATING N-TERMINAL DOMAIN,  
 3 A DNA BINDING DOMAIN AND A TERMINAL STEREOL BINDING DOMAIN.  
 4 THE STEREOL BINDING DOMAIN IS INVOLVED IN THE REGULATION OF  
 5 LIPID METABOLISM. IN THE ABSENCE OF LIGAND, STEREOL BINDING  
 6 ARE FOUND IN THE NUCLEUS ASSOCIATED WITH NUCLEAR COMPONENTS  
 7 HOMER BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE  
 8 HOMER BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE  
 9 STEREOL BINDING DOMAIN IS INVOLVED IN THE REGULATION OF  
 10 STEREOL BINDING. STEREOL BINDING DOMAIN.  
 11 NUCLEUS.  
 12  
 13 THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration  
 14 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 15 at the European Bioinformatics Institute. There are no restrictions on its  
 16 use by non-profit institutions as long as its content is in no way  
 17 modified and this statement is not removed, usage by and for commercial  
 18 entities requires a license agreement (See <http://www.ebi.ac.uk/ebd/sequence>  
 19 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 20  
 21 EMBL: Y00102; CAA69287.1;  
 22 EMBL: X61096; CAA44111.1;  
 23 EMBL: S61779; CAA44111.1;  
 24 EMBL: P03472; U00001;  
 25 EMBL: P03472; U00001;  
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 196 EMBL: P03472; U00001;  
 197 EMBL: P03472; U00001;  
 198 EMBL: P03472; U00001;  
 199 EMBL: P03472; U00001;  
 200 EMBL: P03472; U00001;



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•



142 N. J. J. VAN ALPHEN

CC DNA encoding estrogen receptor - useful in screening assay to  
 CC identify novel ligands or hormonal analogues.

XX Claim 4: Page 45-47; 45pp; English.

XX This sequence represents a novel estrogen binding protein isolated from  
 CC human testis cDNA in order to study estrogen-receptor transition initiation  
 CC codons using 5' RACE-PCR technology. This receptor is able to bind and  
 CC be activated by estradiol, estrone and estrifol, can be used in a screening  
 CC assay for the identification of new drugs e.g. novel ligands or hormonal  
 CC analogues.

XX Sequence: 540 AA:

Query Match: 100.0%; Score 1181; DB ID: Length 540;  
 Host Local Similarity: 100.0%; Prod. No. 4.36-122;  
 Matches: 234; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 LVLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 60  
 266 LVLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 120  
 428 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 180  
 590 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 240  
 752 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 300  
 914 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 360  
 1076 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 420  
 1238 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 480  
 1400 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 540

XX AAW7658 standard; Protein: 540 AA.

XX AAW7658: 07-JUN-1999 (first entry)

XX Human estrogen receptor-beta.

XX Estrogen receptor-beta; ER-beta; human.

XX Homo sapiens.

XX W0907847 AL.

XX 14-FEB-1999.

XX 20-SEP-2001: 98W-0814944.

XX 15-MAR-2001: 2001W-0808276.

XX 15-MAR-2001: 2001W-0808276.

XX (AMMP) AMERICAN NMME Prod Comp.

XX Blat RA, Henderson RA, Hsiao C, Karathanasis SK;

XX WPI: 1999-167424/14.

XX N-ESTR: AAX-164.

XX Human estrogen receptor-beta coding sequence - useful in the

XX production of human estrogen receptor-beta and identification of

XX human estrogen receptor-beta interactive compounds

XX Claim 17: Page 42-44; 49pp; English.

XX This polypeptide comprises a full-length human estrogen receptor-beta

XX (ER-beta), including 45 previously unknown N-terminal amino acids.

CC residues that are believed to contribute to the transcription

CC activation function of the receptor. The amino acid sequence was

CC deduced from the nucleotide sequence (see AAX2464) of an isolated

CC cDNA clone. ER-beta is selectively expressed in the thymus,

CC spleen, ovary and testes. The invention encompasses ER-beta

CC polypeptides and polypeptides, particularly peptides which

CC include residues 1-45 of ER-beta. The invention also provides

CC expression systems in which transcriptionally active ER-beta or

CC ER-beta can be produced, as well as screening methods for

CC identifying ER-beta agonists and antagonists (including

CC tissue-specific agonists and anti-estrogens), and ER-beta

CC co-activators and inhibitors.

XX Sequence: 540 AA:

Query Match: 100.0%; Score 1181; DB ID: Length 540;  
 Host Local Similarity: 100.0%; Prod. No. 4.36-122;  
 Matches: 234; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 LVLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 60  
 266 LVLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 120  
 428 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 180  
 590 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 240  
 752 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 300  
 914 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 360  
 1076 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 420  
 1238 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 480  
 1400 VLLLEAPPPHVLISPSAPFTASMMSTTRKATRELVIMISWAKIPGVEVSTFPG 540

XX AAE10457 standard; Protein: 540 AA.

XX AAE10457: 18-DEC-2001 (first entry)

XX Human estrogen receptor (ER)-beta protein.

XX Estrogen receptor-beta; dietary compound; environmental pollutant;

XX rod wine; ER-beta mediated cell growth inhibition modulator; human.

XX Homo sapiens.

XX W0200169262-A1.

XX 20-SEP-2001.

XX 15-MAR-2001: 2001W-0808276.

XX 15-MAR-2001: 2001W-0808276.

XX (DYMA-1) UNIV MASSACHUSETTS.

XX WPI: 2001-546920/67.

XX N-ESTR: AAD18442.

XX In vitro screening for modulator of estrogen receptor-beta-mediated

XX cell growth inhibition by contact and cell having functional ER-beta

XX protein with candidate compound and detecting ER-beta regulated gene

XX expression

XX Example 2, Fig 7A; 49pp; English.

XX













```

18 001. 1999-142852/12.
XX
XX Human oestrogen receptor beta-4 - useful in treating and monitoring
XX tumours
XX
XX Example 2: Fig 2b; Supp: English.
XX
XX The present sequence is alternatively spliced isoform mER beta 2
XX of the murine complete oestrogen receptor-beta (ER beta-c), or
XX mER beta-3). The mER beta 3 gene (see AAX24935) contains 9 exons,
XX including the newly described exon 5B, which is not found in ER
XX beta-1. Exon 5B is located in the ligand binding domain of mER
XX beta-3, and probably plays a significant role in mER beta-3 function.
XX The mER beta-2 clone was isolated from an embryonic stem cell
XX genomic library. It covers exon 3, 2 other isoforms, mER beta-1
XX (see AAW98125) and rat ER beta 4 (see AAW98127), have also been
XX isolated, and the human exon 5B region (see AAX24934) has been
XX identified. Based on these sequences, the invention provides
XX methods for identifying agents that block or augment ER beta-c
XX mediated transcriptional regulation, methods to determine whether
XX ER beta-c or its isoforms is being expressed in tissues or cells,
XX and methods of identifying and using agents that block the
XX transcriptional regulation of genes by ER beta-3 or its isoforms,
XX which in turn modulates other biological and pathological
XX processes. Gene therapy expression of ER beta-c is envisaged.
XX
XX Sequence 510 AA:
XX
XX Query Match 94.0%; Score 1110; FR 20; Length 510;
XX Post local similarity 92.7%; Prot No 36-114;
XX Matches 216; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
XX
XX 1 LVLTLEAPPPHVLISPSAPPTFASMMNSIKIAKEIVHMTSMKRIQGVNLSIFNQ 60
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 218 IETLLEGGTFNVRSPSPFLEISMMNSIKIAKELTSMGKIPGVNLSIDQ 107
XX
XX 61 VLLIESCMEEVLMGKLMKRSIDHPKRIIPADYIMDKRKVEGHEIFDMILATSPR 120
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 200 VLLIESCMEEVLMGKLMKRSIDHPKRIIPADYIMDKRKVEGHEIFDMILATSPR 167
XX
XX 121 PEIKLQHEVEYCVKAMHINSNMPVATGFAUSPEKIAHNAVITDAVWYIARSGIS 180
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 200 VLLIESCMEEVLMGKLMKRSIDHPKRIIPADYIMDKRKVEGHEIFDMILATSPR 167
XX
XX 181 SQQSSMLANIMISIVVIAKSKGMPIIMKRNKVVPEYDILEMNAHVI 233
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 428 SIIPTIADLITISHTVIGSKIMVLLIGVAKKGVPGYDILLEMNAHVI 180
XX
XX RESULT 17
XX AA00125 standard; Protein: 549 AA
XX
XX AA00125.
XX
XX 21 JUN-1999 (first entry)
XX
XX Mouse oestrogen receptor beta isoform mER beta-1.
XX
XX Oestrogen receptor; ER beta-1; ER beta-c; mouse; tumour;
XX diagnosis; therapy; isoform.
XX
XX Mus musculus.
XX
XX W09905170 A1.
XX
XX 04-FEB-1999.
XX
XX 28-JUN-1998; 98W01-0815539.
XX
XX 30-JUL-1997; 97US-0054210.
XX
XX 28-JUL-1997; 97US-0053869.
XX

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XX
XX (OYVA ) UNIV YALE.
XX
XX Denton R, Fraston C, Gallen R, Rische-Ridon M;
XX
XX W01. 1999-142852/12.
XX
XX Human oestrogen receptor beta-4 - useful in treating and monitoring
XX tumours
XX
XX Example 2: Fig 2a; 89pp; English.
XX
XX The present sequence is alternatively spliced isoform mER beta-1
XX of the murine complete oestrogen receptor-beta (ER beta-c), or
XX mER beta-3). The mER beta-3 gene (see AAX24935) contains 9 exons,
XX including the newly described exon 5B, which is not found in ER
XX beta-1. Exon 5B is located in the ligand binding domain of mER
XX beta-3, and probably plays a significant role in mER beta-3 function.
XX The mER beta-1 clone was isolated by PCR of mRNA, and by
XX amplification from a mouse embryonic stem cell genomic DNA library.
XX It lacks exon 5B. Preliminary data indicate that the mER beta-1
XX isoform may be more active than the full-length mER beta-3 (see
XX AAW98128). 2 other isoforms, mER beta 2 (see AAW98126) and rat ER
XX beta-4 (see AAW98127), have also been isolated, and the human 5B
XX region (see AAX24934) has been identified. Based on these sequences,
XX the invention provides methods for identifying agents that block or
XX augment ER beta-c mediated transcriptional regulation, methods to
XX determine whether ER beta-c or its isoforms is being expressed in
XX tissues or cells, and methods of identifying and using agents that
XX block the transcriptional regulation of genes by ER beta-c or its
XX isoforms, which in turn modulates other biological and pathological
XX processes. Gene therapy expression of ER beta-c is envisaged.
XX
XX Sequence 549 AA:
XX
XX Query Match 94.0%; Score 1110; FR 20; Length 549;
XX Post local similarity 92.7%; Prot No 36-114;
XX Matches 216; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
XX
XX 1 LVLTLEAPPPHVLISPSAPPTFASMMNSIKIAKEIVHMTSMKRIQGVNLSIFNQ 60
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 287 IETLLEGGTFNVRSPSPFLEISMMNSIKIAKELTSMGKIPGVNLSIDQ 146
XX
XX 61 VLLIESCMEEVLMGKLMKRSIDHPKRIIPADYIMDKRKVEGHEIFDMILATSPR 120
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 347 VLLIESCMEEVLMGKLMKRSIDHPKRIIPADYIMDKRKVEGHEIFDMILATSPR 167
XX
XX 121 PEIKLQHEVEYCVKAMHINSNMPVATGFAUSPEKIAHNAVITDAVWYIARSGIS 180
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 407 IETLLEGGTFNVRSPSPFLEISMMNSIKIAKELTSMGKIPGVNLSIDQ 146
XX
XX 181 SQQSSMLANIMISIVVIAKSKGMPIIMKRNKVVPEYDILEMNAHVI 233
XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
XX 467 SIIPTIADLITISHTVIGSKIMVLLIGVAKKGVPGYDILLEMNAHVI 180
XX
XX 467 SIIPTIADLITISHTVIGSKIMVLLIGVAKKGVPGYDILLEMNAHVI 180
XX
XX RESULT 17
XX AA004434 standard; Protein: 549 AA.
XX
XX AA004434.
XX
XX 25 JUN 1999 (first entry)
XX
XX Murine mER beta-1 clone protein sequence.
XX
XX Estrogen receptor beta; oestrogen receptor beta; ER beta.
XX
XX Mus sp.
XX
XX W09905171 A1.
XX

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XX estrogen receptor mediated disease; complex; ligand antagonist;  
 XX Homo sapiens;  
 XX OS628990-B1;  
 XX -08 MAY-2001;  
 XX 12-FEB-1999; 9908-024945;  
 XX 13-FEB-1998; 9808-0000972;  
 XX (KARA) KARA HIO AB;  
 XX Bjornaren J, Thorsell A, Engstrom O, Bonn T, Carlquist M;  
 XX Bjornowski AM, Piles A-W, Holthoff HF;  
 XX W01:401-416591/44;  
 XX Abstracts comprising amino acids of the estrogen-receptor beta ligand  
 XX binding domain complexed with an antagonistic ligand, useful for the  
 XX treatment of estrogen receptor mediated diseases in females;  
 XX Claim 9: Column 9-12; 21pp; English.

The invention relates to crystals comprising at least 150 amino acid  
 residues of the estrogen receptor beta (ERbeta) ligand binding domain  
 complexed with a ligand which is an antagonist or partial antagonist.  
 The crystals may be used to inhibit the activity of estradiol  
 (or mimetics) by providing ligands which bind to ERbeta with a high  
 affinity, blocking the activity of estradiol. Alternatively, binding of  
 the ligand to ERbeta may cause conformational changes to ERbeta, thus  
 inhibiting further binding to it. Therefore, the ligands are useful in  
 the treatment of estrogen receptor mediated diseases in females.  
 The present sequence is the protein sequence of a crystal of human  
 ERbeta ligand binding domain complexed with gonestrolin.

Sequence: 229 AA;

Query Match 92.4%; Score 1091.5; DB 20; Length 229;  
 Best Local Similarity 94.8%; Prev. No. 1 to 112;  
 Matches 221; Conservative 0; Mismatches 1; Indels 11; Gaps 2;

QY 1 LVLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 60  
 DB |||||  
 QY 6 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 60  
 DB |||||  
 QY 61 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 120  
 DB |||||  
 QY 63 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 122  
 DB |||||  
 QY 121 RELKQREKYLVRAMLLNSSMELVTAQAVSSKRIALLINAVLDALWVIANSGIS 180  
 DB |||||  
 QY 122 RELKQREKYLVRAMLLNSSMELVTAQAVSSKRIALLINAVLDALWVIANSGIS 180  
 DB |||||  
 QY 141 SGGSSMLPLANILMLSHVRIASNGSMELLMKCKNVVPVVDLLEMLNAHVL 234  
 DB |||||  
 QY 177 SPPISMLANILMLSHVRIASNGSMELLMKCKNVVPVVDLLEMLNAHVL 229  
 DB |||||

RESULT 20

AAV4433  
 ID AAV4433 standard; Protein: 560 AA.

XX AAV4433;

XX 25-JUN-1999 (first entry)

XX Mouse mER beta-3 clone protein sequence.

XX estrogen receptor beta; estrogen receptor beta; ER beta.

OS Mus sp.  
 XX W09905171-A1;  
 XX 04-FEB-1999;  
 XX 28-JUL-1998; 98WD-US15540;  
 XX 30-JUL-1997; 97US-0054210;  
 XX 28-JUL-1997; 97US-0054865;  
 XX (UYVA) UYVA YALF;  
 XX Baron R, Chanton B, Benton R, Jopson S, Garnier J;  
 XX W01:1999-14-05/12;  
 XX N-PSDB: AAX33382;  
 XX Novel murine estrogen receptor beta genes and splice variants  
 XX useful for treating estrogen receptor-beta mediated disorders  
 XX Claim 9: Fig 1b-1; 89pp; English.

The present sequence is the murine complete estrogen receptor beta  
 (mER beta c) also designated mER beta-3). The protein can be used to  
 screen for agents that modulate or block the interaction between the  
 ER beta c protein and physiologically, stilbene or 11phenylethylene  
 (anti)estrogens. The antibody which binds the protein can be used in  
 assays to detect activation of the ER beta protein and can be used for  
 subcellular localization of the protein. The complementary nucleic acid  
 can be used to inhibit expression of the ER beta c nucleic acid.

Sequence: 560 AA;

Query Match 92.4%; Score 1091; DB 20; Length 560;  
 Best Local Similarity 86.1%; Prev. No. 4,46-112;  
 Matches 216; Conservative 10; Mismatches 7; Indels 18; Gaps 1;

QY 1 LVLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 60  
 DB |||||  
 QY 287 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 406  
 DB |||||  
 QY 61 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 102  
 DB |||||  
 QY 347 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 406  
 DB |||||  
 QY 103 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 162  
 DB |||||  
 QY 407 VLLLEAPPHVILSRSAFTASMMMSITRIAKELVHMSWAKITGVPSLSTFG 406  
 DB |||||  
 QY 121 RELKQREKYLVRAMLLNSSMELVTAQAVSSKRIALLINAVLDALWVIANSGIS 232  
 DB |||||  
 QY 467 INVDALWVIANSGIS 232  
 DB |||||  
 QY 223 LLEMLNAHVL 234  
 DB |||||  
 QY 527 LLEMLNAHVL 537  
 DB |||||

RESULT 21

AAW98128  
 ID AAW98128 standard; Protein: 567 AA.

XX AAW98128;

XX 21-JUN-1999 (first entry)

XX Mouse complete estrogen receptor beta mER beta 4.

XX estrogen receptor; ER beta 4; ER beta c; mouse; tumour;

XX















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Model	Photo. No.
1	100
2	101
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100	199

DE: ESTROGEN RECEPTOR-RELATED PROTEIN.

















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Q7 51 VP ESCMHEV MCM MMS TONGK

DB 284 VALLSFWMEVIMMWSKIDHCKLFAHDIWIDDEKXVIGLLEEDMLATISRE 442  
 07 121 PRLKRGHBYVYVAMTLENSMYPVAVYDMSKRLANLNAVDAVWVIASSGIS 180  
 10 434 TLKZGHEVYVYVAMTLENSMYPVAVYDMSKRLANLNAVDAVWVIASSGIS 182  
 07 141 SDOGSMBANLMLSHVBNRSGRPHLEMSKRNHVEYVHLLLSMNAHV 234  
 10 404 SDOGSMBANLMLSHVBNRSGRPHLEMSKRNHVEYVHLLLSMNAHV 455

RESULT 4  
 US OR 86-620A 14  
 1 Sequence 1: Application No. 622015  
 2 Patent No. 622015  
 3 GENERAL INFORMATION  
 4 APPLICANT: WILKINSON, HILARY  
 5 TITLE OF INVENTION: DISTORTION PROTECTOR  
 6 FILING DATE: 2004.7  
 7 PRIORITY APPLICATION NUMBER: 2004/0109 617  
 8 CURRENT FILING DATE: 1998 08 25  
 9 PRIORITY APPLICATION NUMBER: 60/050 271  
 10 EXAMINER FILING DATE: 1997 09 08  
 11 EXAMINER APPLICATION NUMBER: 60/066 520  
 12 EXAMINER FILING DATE: 1997 09 10  
 13 NUMBER OF SEQ TO NOS: 22  
 14 SOFTWARE: FastSeq for Windows Version 4.0  
 15 SEQ TO NO: 1  
 16 LENGTH: 548  
 17 TYPE: PPT  
 18 ORIGINATOR: HERRAH  
 19 US OR 86-620 1

Query Match 100.0% Score 1111 DB 4 Length 548  
 Best Local Similarity 100.0% Prod. No. 1 200 145  
 Matches 2172 Conserved 82 Mismatches 82 Indels 05 Gaps 02

07 1 EVTLLEAPRVLSPVATFASMSKSTKLAKELVHMSKAFDEVEISLFG 60  
 10 280 EVTLLEAPRVLSPVATFASMSKSTKLAKELVHMSKAFDEVEISLFG 282  
 07 61 VLLSFWMEVIMMWSKIDHCKLFAHDIWIDDEKXVIGLLEEDMLATISRE 120  
 10 434 VLLSFWMEVIMMWSKIDHCKLFAHDIWIDDEKXVIGLLEEDMLATISRE 435  
 07 121 PRLKRGHBYVYVAMTLENSMYPVAVYDMSKRLANLNAVDAVWVIASSGIS 180  
 10 434 TLKZGHEVYVYVAMTLENSMYPVAVYDMSKRLANLNAVDAVWVIASSGIS 182  
 07 141 SDOGSMBANLMLSHVBNRSGRPHLEMSKRNHVEYVHLLLSMNAHV 234  
 10 404 SDOGSMBANLMLSHVBNRSGRPHLEMSKRNHVEYVHLLLSMNAHV 455

RESULT 4  
 US OR 86-620A 14  
 1 Sequence 1: Application No. 622015  
 2 Patent No. 622015  
 3 GENERAL INFORMATION  
 4 APPLICANT:  
 5 TITLE OF INVENTION: orphan receptor  
 6 NUMBER OF SEQUENCES: 19  
 7 COMPUTER RELEVABLE PDBR:  
 8 MEDIUM TYPE: floppy disk  
 9 COMPUTER: IBM pc compatible  
 10 OPERATING SYSTEM: pc dos/ms dos  
 11 SOFTWARE: Patent In Release #1.0, Version #1.25 (PPT)  
 12 CURRENT APPLICATION DATA:  
 13 FILING DATE: 95/08/28/06 620A  
 14 PRIOR APPLICATION DATA:  
 15 FILING DATE: 95/08/28/06 620A  
 16 APPLICATION NUMBER: 622015/06 620A

07 FILING DATE:  
 1 APPLICATION NUMBER: GB 9518272.1  
 2 FILING DATE: 08-SEP-1995  
 3 PRIOR APPLICATION DATA:  
 4 FILING DATE: 15-MAR-1996  
 5 FILING DATE: 15-MAR-1996  
 6 FILING DATE: 15-MAR-1996  
 7 APPLICATION NUMBER: GB 9607542.0  
 8 FILING DATE: 11-APR-1996  
 9 PRIOR APPLICATION DATA:  
 10 APPLICATION NUMBER: GB 9609576.5  
 11 FILING DATE: 08-MAY-1996  
 12 INFORMATION FOR SEQ TO NOS: 145  
 13 SEQUENCE CHARACTERISTICS:  
 14 LENGTH: 484 amino acids  
 15 TYPE: amino acid  
 16 TOPOLOGY: linear  
 17 ORIGIN: Source:  
 18 ORGANISM: Rattus rattus  
 19 US OR 86-620A 14

Query Match 94.1% Score 1111 DB 2 Length 484  
 Best Local Similarity 94.1% Prod. No. 428 125  
 Matches 2172 Conserved 82 Mismatches 82 Indels 05 Gaps 02

07 1 EVTLLEAPRVLSPVATFASMSKSTKLAKELVHMSKAFDEVEISLFG 60  
 10 280 EVTLLEAPRVLSPVATFASMSKSTKLAKELVHMSKAFDEVEISLFG 282  
 07 61 VLLSFWMEVIMMWSKIDHCKLFAHDIWIDDEKXVIGLLEEDMLATISRE 120  
 10 434 VLLSFWMEVIMMWSKIDHCKLFAHDIWIDDEKXVIGLLEEDMLATISRE 435  
 07 121 PRLKRGHBYVYVAMTLENSMYPVAVYDMSKRLANLNAVDAVWVIASSGIS 180  
 10 434 TLKZGHEVYVYVAMTLENSMYPVAVYDMSKRLANLNAVDAVWVIASSGIS 182  
 07 141 SDOGSMBANLMLSHVBNRSGRPHLEMSKRNHVEYVHLLLSMNAHV 234  
 10 404 SDOGSMBANLMLSHVBNRSGRPHLEMSKRNHVEYVHLLLSMNAHV 455

RESULT 4  
 US OR 86-620A 2  
 1 Sequence 2: Application No. 622015  
 2 Patent No. 622015  
 3 GENERAL INFORMATION  
 4 APPLICANT:  
 5 TITLE OF INVENTION: orphan receptor  
 6 NUMBER OF SEQUENCES: 19  
 7 COMPUTER RELEVABLE PDBR:  
 8 MEDIUM TYPE: floppy disk  
 9 COMPUTER: IBM pc compatible  
 10 OPERATING SYSTEM: pc dos/ms dos  
 11 SOFTWARE: Patent In Release #1.0, Version #1.25 (PPT)  
 12 CURRENT APPLICATION DATA:  
 13 FILING DATE: 95/08/28/06 620A  
 14 PRIOR APPLICATION DATA:  
 15 FILING DATE: 95/08/28/06 620A  
 16 APPLICATION NUMBER: 622015/06 620A  
 17 FILING DATE: 95/08/28/06 620A  
 18 PRIOR APPLICATION DATA:  
 19 FILING DATE: 95/08/28/06 620A  
 20 APPLICATION NUMBER: 622015/06 620A  
 21 FILING DATE: 95/08/28/06 620A  
 22 APPLICATION NUMBER: 622015/06 620A  
 23 FILING DATE: 95/08/28/06 620A  
 24 APPLICATION NUMBER: 622015/06 620A  
 25 FILING DATE: 95/08/28/06 620A  
 26 APPLICATION NUMBER: 622015/06 620A  
 27 FILING DATE: 95/08/28/06 620A  
 28 APPLICATION NUMBER: 622015/06 620A  
 29 FILING DATE: 95/08/28/06 620A  
 30 APPLICATION NUMBER: 622015/06 620A

INFORMATION FOR SFO ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Ratios ratios  
US-08-826-620A 2

Query Match: 94.1% Score 1111, DB 2, Length 485  
Post Local Similarity: 94.1% Pred. No. 4,20-123;  
Matches 214, Conservative 10, Mismatches 9, Indels 0, Gaps 0

1 LVLTLEAEPPHVLISRSAPFTFASMMSSITFASPPVHVSQVAKTVEGTLFEDMLATSPF 60  
|||||  
223 LVLTLEAEPPHVLISRSAPFTFASMMSSITFASPPVHVSQVAKTVEGTLFEDMLATSPF 282  
61 VLLLESTWMEVLMWGLMWSLIDHDKLIFADPVLIDHDKVEGTLFEDMLATSPF 120  
|||||  
283 VLLLESTWMEVLMWGLMWSLIDHDKLIFADPVLIDHDKVEGTLFEDMLATSPF 342  
121 PPTFAPVYVAVAMHNSAPFTVTAZASAPVHVSQVAKTVEGTLFEDMLATSPF 180  
|||||  
443 PPTFAPVYVAVAMHNSAPFTVTAZASAPVHVSQVAKTVEGTLFEDMLATSPF 402  
141 SQQSSPMATFMSVAPLNSKQKQTLDMCKHVVVYDLEEMANAVI 243  
|||||  
403 SQQSSPMATFMSVAPLNSKQKQTLDMCKHVVVYDLEEMANAVI 465

# RESULT 5

US-08-826-620A 14  
Sequence 5, Application US/08846620A  
Patent No. 6958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER RELEASABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM pc compatible  
SOFTWARE SYSTEM: PC-POS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 85-072849, 620A  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 17/EP96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9607542.0  
FILING DATE: 11-APR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SFO ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 484 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
US-08-826-620A 14

Query Match: 92.5% Score 1097, DB 2, Length 484,  
Post Local Similarity: 91.8% Pred. No. 6,16-123;

Matches 214, Conservative 10, Mismatches 9, Indels 0, Gaps 0

223 LVLTLEAEPPHVLISRSAPFTFASMMSSITFASPPVHVSQVAKTVEGTLFEDMLATSPF 60  
|||||  
223 LVLTLEAEPPHVLISRSAPFTFASMMSSITFASPPVHVSQVAKTVEGTLFEDMLATSPF 282  
61 VLLLESTWMEVLMWGLMWSLIDHDKLIFADPVLIDHDKVEGTLFEDMLATSPF 120  
|||||  
283 VLLLESTWMEVLMWGLMWSLIDHDKLIFADPVLIDHDKVEGTLFEDMLATSPF 342  
121 PPTFAPVYVAVAMHNSAPFTVTAZASAPVHVSQVAKTVEGTLFEDMLATSPF 180  
|||||  
443 PPTFAPVYVAVAMHNSAPFTVTAZASAPVHVSQVAKTVEGTLFEDMLATSPF 402  
141 SQQSSPMATFMSVAPLNSKQKQTLDMCKHVVVYDLEEMANAVI 243  
|||||  
403 SQQSSPMATFMSVAPLNSKQKQTLDMCKHVVVYDLEEMANAVI 465  
RESULT 6  
US-08-826-620A 5  
Sequence 5, Application US/08846620A  
Patent No. 6958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER RELEASABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM pc compatible  
SOFTWARE SYSTEM: PC-POS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 85-072849, 620A  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 17/EP96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9607542.0  
FILING DATE: 11-APR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SFO ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
US-08-826-620A 5

Query Match: 92.5% Score 1097, DB 2, Length 485,  
Post Local Similarity: 91.8% Pred. No. 6,20-123;  
Matches 214, Conservative 10, Mismatches 9, Indels 0, Gaps 0

61 VLLLESTWMEVLMWGLMWSLIDHDKLIFADPVLIDHDKVEGTLFEDMLATSPF 120  
|||||  
283 VLLLESTWMEVLMWGLMWSLIDHDKLIFADPVLIDHDKVEGTLFEDMLATSPF 342  
121 PPTFAPVYVAVAMHNSAPFTVTAZASAPVHVSQVAKTVEGTLFEDMLATSPF 180  
|||||





















Sequence 14: Application US/08764870  
 Patent No. 6,266,446

PERSONAL INFORMATION:

APPLICANT: Scanlan, Thomas S  
 APPLICANT: Baxley, John D  
 APPLICANT: Fletcher, Robert J  
 APPLICANT: Womack, Richard L  
 APPLICANT: Koshnoff, Peter J  
 APPLICANT: Apfelter, James W  
 APPLICANT: West, Brian  
 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
 TITLE OF INVENTION: Binding Domains  
 NUMBER OF SEQUENCES: 16  
 ADDRESSING ADDRESS:  
 STREET: Cooley Goddard  
 STREET: Five Palo Alto Square, 3000 El Camino Real  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306

OTHER READABLE FORM:

MEDIA TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.10  
 NUPRI APPLICATION DATA:  
 APPLICATION NUMBER: US-2002/0764,870  
 FILING DATE: 14-Dec-1996  
 CLASSIFICATION: 530

OTHER APPLICATION DATA:

APPLICATION NUMBER: US 60/008,540  
 FILING DATE: 14-Dec-1995  
 OTHER APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,543  
 FILING DATE: 14-Dec-1995

OTHER APPLICATION DATA:

APPLICATION NUMBER: US 60/008,606  
 FILING DATE: 14-Dec-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nakamura, Jackie N  
 REGISTRATION NUMBER: 49,966  
 REFERENCE: 1,106,803, 2,115,010US  
 TELEPHONE: (650)843-6000  
 TELEPHONE: (650)843-6000

SEQUENCE CHARACTERISTICS:

LENGTH: 943 amino acids  
 TYPE: amino acid  
 STRANDNESS:  
 topology: linear  
 MOTIF TYPE: protein  
 US-08-764,870 14

Query Match:

Post local similarity: 29.48; Score 240.5; DB 4; Length 933;  
 Mismatches 58; conservative 46; Mismatches 82; Indels 11; Gaps 6;

1 LVLLLEAFPHVLSVSA PPTFASMMSTKAEIVMSQAKIPVSLSD 59  
 60 VPTLESVMVLMQIMESIDHG -KLFAFDVIDRDEKCEVGHLEPDLIAIT 117  
 747 QILLVSMWGVVWVSWSTYKVSQMLTATLLENLEME-ESSTSLCTIMQIT 805  
 118 SEPEKRGHNVGVAMILNS SMYVVAQ-VAISKRIAHJNAVTAIVVIA 175  
 119 VEVVAVVETTCVAVTITNTELENG-LEFEMESYIEELFA---TDLQ 860  
 176 KSLSSQSSQSMANIL 192  
 861 KVVSSSQVYVJIKIL 877

Search completed: July 12, 2002, 14:46:11  
 Job time: 119 sec

\* \* \*





[illegible]

1924/Middleton et al. / Hospital's (SOP) (evaluation) status production

Match	6/2	7/2	8/2	9/2	10/2	11/2	12/2	13/2	14/2	15/2	16/2	17/2	18/2	19/2	20/2	21/2	22/2	23/2	24/2	25/2	26/2	27/2	28/2	29/2	30/2	31/2	32/2	33/2	34/2	35/2	36/2	37/2	38/2	39/2	40/2	41/2	42/2	43/2	44/2	45/2	46/2	47/2	48/2	49/2	50/2	51/2	52/2	53/2	54/2	55/2	56/2	57/2	58/2	59/2	60/2	61/2	62/2	63/2	64/2	65/2	66/2	67/2	68/2	69/2	70/2	71/2	72/2	73/2	74/2	75/2	76/2	77/2	78/2	79/2	80/2	81/2	82/2	83/2	84/2	85/2	86/2	87/2	88/2	89/2	90/2	91/2	92/2	93/2	94/2	95/2	96/2	97/2	98/2	99/2	100/2
Matches	6/2	7/2	8/2	9/2	10/2	11/2	12/2	13/2	14/2	15/2	16/2	17/2	18/2	19/2	20/2	21/2	22/2	23/2	24/2	25/2	26/2	27/2	28/2	29/2	30/2	31/2	32/2	33/2	34/2	35/2	36/2	37/2	38/2	39/2	40/2	41/2	42/2	43/2	44/2	45/2	46/2	47/2	48/2	49/2	50/2	51/2	52/2	53/2	54/2	55/2	56/2	57/2	58/2	59/2	60/2	61/2	62/2	63/2	64/2	65/2	66/2	67/2	68/2	69/2	70/2	71/2	72/2	73/2	74/2	75/2	76/2	77/2	78/2	79/2	80/2	81/2	82/2	83/2	84/2	85/2	86/2	87/2	88/2	89/2	90/2	91/2	92/2	93/2	94/2	95/2	96/2	97/2	98/2	99/2	100/2

[illegible]

## 10E, 240)

RESULT	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100			
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

2. Specimens submitted (check one)  
 (a) ☐ *For* Mar-1992 submission 14 Jul 1994 11:01 AM (date & time)  
 (b) ☐ *For* Mar-1992 submission 14 Jul 1994 11:01 AM (date & time)  
 (c) ☐ *For* Mar-1992 submission 14 Jul 1994 11:01 AM (date & time)

62. Accession: A4034; S07192  
R. Maxwell, B. Lee, M. J. McPartland, D. J. C. Macdonald, F. W. C. Brown, G. L. G. M. Hall  
Environ Biol Fish 1: 35-45, 1987

Mol. Endocrinol. 1, 25-35, 1987.  
Attlee, S. Structural organization and regulation of the chicken estrogen receptor. A. Kottmann, R. M. Attlee, and M. D. Mittleman. In: *Estrogen and Estrogen Receptors*, Ed. by J. L. Garavito, pp. 1-12. Academic Press, New York, 1986.

A: ketone group: A40914; M110:884162.  
A: Acetone: A40914

A<sub>2</sub> Molecule Type: mRNA  
A<sub>3</sub> Residues: 1-589 - MAX

A. Kottmann, *Journal of Molecular Biology* 307:102 (1997).

A: Molecular type: mKNA  
A: Residues: 1-256, 47, 258-589, KRH  
Accession: F010098; EMBL: X03805; NID: 063478; PIR: AA274344; PIR: 063800  
The above sequence is a full-length cDNA deposited into the

<sup>2</sup>Comment: The steroid hormones and their receptors are involved in the regulation of gene expression. In the absence of ligand, steroid hormone receptors are thought to be weak transcription factors. Upon binding of ligand, steroid hormone receptors are thought to be strong transcription factors.

complex appears to recognize discrete DNA sequences upstream of transcription start sites. Superficially, estrogen receptor (erbA) transforming protein homology 2, which is known to bind to DNA, might have also been involved in steroid binding, steroid formation, or steroid release.

## E: 171-2611

F7.177-200/koq/qom; zinc finger cccc motif  
 F7.213-239/koq/qom; zinc finger cccc motif  
 F7.250-265/koq/qom; nuclear localization signal  
 F7.294-543/koq/qom; steroid binding #status predicted - SIB

170	182	186	190	194	198	202	206	210	214	218	222	226	230	234	238	242	246	250	254	258	262	266	270	274	278	282	286	290	294	298	302	306	310	314	318	322	326	330	334	338	342	346	350	354	358	362	366	370	374	378	382	386	390	394	398	402	406	410	414	418	422	426	430	434	438	442	446	450	454	458	462	466	470	474	478	482	486	490	494	498	502	506	510	514	518	522	526	530	534	538	542	546	550	554	558	562	566	570	574	578	582	586	590	594	598	602	606	610	614	618	622	626	630	634	638	642	646	650	654	658	662	666	670	674	678	682	686	690	694	698	702	706	710	714	718	722	726	730	734	738	742	746	750	754	758	762	766	770	774	778	782	786	790	794	798	802	806	810	814	818	822	826	830	834	838	842	846	850	854	858	862	866	870	874	878	882	886	890	894	898	902	906	910	914	918	922	926	930	934	938	942	946	950	954	958	962	966	970	974	978	982	986	990	994	998	1002	1006	1010	1014	1018	1022	1026	1030	1034	1038	1042	1046	1050	1054	1058	1062	1066	1070	1074	1078	1082	1086	1090	1094	1098	1102	1106	1110	1114	1118	1122	1126	1130	1134	1138	1142	1146	1150	1154	1158	1162	1166	1170	1174	1178	1182	1186	1190	1194	1198	1202	1206	1210	1214	1218	1222	1226	1230	1234	1238	1242	1246	1250	1254	1258	1262	1266	1270	1274	1278	1282	1286	1290	1294	1298	1302	1306	1310	1314	1318	1322	1326	1330	1334	1338	1342	1346	1350	1354	1358	1362	1366	1370	1374	1378	1382	1386	1390	1394	1398	1402	1406	1410	1414	1418	1422	1426	1430	1434	1438	1442	1446	1450	1454	1458	1462	1466	1470	1474	1478	1482	1486	1490	1494	1498	1502	1506	1510	1514	1518	1522	1526	1530	1534	1538	1542	1546	1550	1554	1558	1562	1566	1570	1574	1578	1582	1586	1590	1594	1598	1602	1606	1610	1614	1618	1622	1626	1630	1634	1638	1642	1646	1650	1654	1658	1662	1666	1670	1674	1678	1682	1686	1690	1694	1698	1702	1706	1710	1714	1718	1722	1726	1730	1734	1738	1742	1746	1750	1754	1758	1762	1766	1770	1774	1778	1782	1786	1790	1794	1798	1802	1806	1810	1814	1818	1822	1826	1830	1834	1838	1842	1846	1850	1854	1858	1862	1866	1870	1874	1878	1882	1886	1890
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1990-2007 binding sites: phosphate (Ser) (covalent) + status predicted

Copy Match: 98.4%; Score 800; Job 1; Length 589;

best local similarity	97.08	Prod. No. 1, Inc	41
Matthias	64; (conservative)	Z; Mischak's	02
		Indels	07
		Pages	27

1. GAMMA-VARIATION OF THE RADIATION-INDUCED POLYMERIZATION OF 1,3,5-TRIMETHYLBENZENE 60

170 VAN DER AART, A. M., and J. H. VAN DER MEULEN. 1978. The effects of  
171  
172

$\Omega_Y$	$\epsilon_1$
	$1^{\vee}; M; M$
	$\epsilon_1 \epsilon_1$
	$1^{\vee} 1^{\vee}$
	$1^{\vee} 1$
	$1 1^{\vee}$
	$1 1$

244 YYYCM 244





1000

## RESULTS

### Practical 1









Cispeptide: Homo Sapiens (man)

Cloned: 04-Jan-1986 #sequence: revision 04-Jan-1986 #text\_change 21-Jul-2000

Accession: 694370; 694379; A0247

Ref: Anderson, S.M.; Weidner, C.; Ong, E.S.; Doreilly, D.; Oro, A.; Lebo, R.; Thompson, N. *Cell* 64:641, 1985

Abstract: Primary structure and expression of a human glucocorticoid receptor

Accession number: A0247; MIM:6092206

Accession: 694370

Accession: 694379

Accession: 694379

Accession: 694379; MIM:6092206

Accession: 694379; MIM:6092206

Accession: 694379; MIM:6092206

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P:452-476/region: zinc finger

Query Match

Best Local Similarity: 59.1%; Score: 246; DB: 1; Length: 771

Mismatches: 39; Conservative: 9; Mismatches: 18; Indels: 0; Gaps: 0

Accession: 694379; MIM:6092206

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Accession: 694379; MIM:6092206











23 61 CYEWM 66  
 24 156 cyewm 161

## RESULT 4

AAV1946  
 ID AAV1946 standard; Protein: 474 AA.

AA AAV1946.

DT 23-JUN-2000 (first entry)

DE bovine ER-beta protein.

XX bovine ER-beta; estrogen receptor beta; anticancer anti-osteoporosis;

KW transcriptional transcription; estrogen dependent transcription; cancer;

KW osteoporosis element; ovary; pregnancy; osteoporosis

XX bovine ER-beta.

XX bovine ER-beta.

XX bovine ER-beta.

XX 27-AUG-1998; 98DE-1039115.

XX 27-AUG-1998; 98DE-1039115.

XX (HHE-) 1HF INST HOEMN & PATENTLANDINGS.

XX Walther N.

XX WP1: 2000-257590/23.

XX N-PSDB: AAV37537.

XX New bovine estrogen beta receptor, useful for identifying specific

XX ligands, potentially used for treating cancer and osteoporosis.

XX Claim 1, Page 9 19; 20pp; German.

XX This invention describes a novel isolated bovine estrogen receptor-beta

XX (ERb) which has anticancer and anti-osteoporosis activity. ERb is a

XX transcriptional transactivator that activates estrogen dependent

XX transcription of genes that include an estrogen response element. It is

XX structurally very active than estrogen receptor alpha (ERa) (also its

XX isoforms and peptides containing its ligand binding domain), nucleic acid

XX (111) encoding them, or vectors and cells containing (111) are used to

XX identify ligands (agonists or antagonists) of ERb, particularly specific

XX ligands that do not bind to the estrogen receptor-alpha. These ligands

XX are potentially useful for treating ERb-associated disorders,

XX particularly cancer of the ovary or prostate, or osteoporosis. This

XX sequence represents the bovine ER beta protein described in the method of

XX the invention.

XX Sequence 474 AA;

## RESULT 5

AAW3212

ID AAW3212 standard; Protein: 477 AA.

AC AAW3212;

DT 20-APR-1998 (first entry)

DE Human estrogen receptor protein.

XX estrogen receptor protein; steroid; alternative splicing; estradiol;

KW estrone, estradiol; screening.

XX Homo sapiens.

XX EP798378-A2.

XX 01-OCT-1997.

XX 25-MAR-1997; 97EP-0206003.

XX 22-NOV-1996; 96EP-0203284.

XX 24-MAR-1996; 96EP-0209850.

XX (ALKU) AKZO NOBEL NV.

XX Dijkema R, Mosselman S;

XX WP1: 1997-473188/44.

XX N-PSDB: AAT88412.

XX DNA encoding estrogen receptor - useful in screening assay to

XX identify novel ligands or hormonal analogues

XX Claim 4: Page 18-20; 45pp; English.

XX This sequence represents a novel estrogen binding protein. The cDNA

XX sequence which encodes this protein can be alternatively spliced

XX resulting in the detection of additional transcripts (see AAT88413).

XX This receptor is able to bind and be activated by estradiol, estrone and

XX estradiol, can be used in a screening assay for the identification of new

XX drugs e.g. novel ligands or hormonal analogues.

XX Sequence 477 AA;

XX

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XX

## RESULT 6

AAW14724

ID AAW14724 standard; Protein: 485 AA.

AC AAW14724;

DT 08-JUN-1997 (first entry)

DE Human estrogen receptor beta (ER-beta).

XX Orphan receptor; estrogen receptor beta; ER-beta;

KW nuclear receptor; prostate cancer; benign prostatic hyperplasia;

KW ovary cancer; cardiovascular disease; osteoporosis;

XX environment; pollutant.

XX Homo sapiens.

XX









July 1964	100.0%	Score 486;	DB 20;	Length 548
Best Local Similarity	100.0%	Pred. No. 5, 1e-34;		

## RESULTS





















GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OR protein - protein search, using SW model

Query: 12 2002 11 4 12 Search time: 20.7 seconds  
(without alignments)  
77.879 Million cell updates/sec

Hit list: 08-08-826-361d-3  
486  
1 CAVSSTVASTVHYGVWWSQV  
KMPYSGVQVAPVYVVM 65

Scoring table:  
Blast0M62  
Gapop: 10 0 Gapext: 0 5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post processing: Maximum Match 98  
Listing first 45 summaries

Database: Issued Patents-AA\*

- 1: 08-08-826-361d-3
- 2: 08-08-826-361d-3
- 3: 08-08-826-361d-3
- 4: 08-08-826-361d-3
- 5: 08-08-826-361d-3
- 6: 08-08-826-361d-3

Pred. No. is the number of results predicted by class 1 to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	384	2	US-08-836-620A-15
2	486	100.0	485	2	US-08-836-620A-3
3	486	100.0	548	4	US-09-139-617-1
4	484	99.2	484	2	US-08-836-620A-14
5	392	99.2	485	2	US-08-836-620A-5
6	391	98.7	466	2	US-08-836-620A-11
7	481	98.7	484	2	US-08-836-620A-13
8	481	98.7	485	2	US-08-836-620A-2
9	380	98.4	66	2	US-09-836-620A-12
10	380	98.4	410	6	5223606-5
11	380	98.4	591	2	US-08-836-620A-17
12	480	98.4	595	4	US-09-041-886-45
13	480	98.4	595	4	US-09-764-870-12
14	480	98.4	595	4	US-08-980-115-12
15	480	98.4	595	4	US-08-836-620A-16
16	276	71.5	418	3	US-09-141-000-6
17	276	71.5	418	3	US-09-141-000-6
18	276	71.5	418	3	US-08-836-620A-19
19	276	71.5	418	3	US-09-041-886-11
20	276	71.5	418	3	US-09-041-886-11
21	276	71.5	418	3	US-09-041-886-11
22	276	71.5	418	3	US-09-041-886-11
23	276	71.5	418	3	US-09-041-886-11
24	276	71.5	418	3	US-09-041-886-11
25	276	71.5	418	3	US-09-041-886-11
26	276	71.5	418	3	US-09-041-886-11
27	276	71.5	418	3	US-09-041-886-11

## ALIGNMENTS

28	236	61.1	89	1	US-08-561 072 3	Sequence 4, Appl 1
29	236	61.1	89	1	US-08-561 072 3	Sequence 4, Appl 1
30	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
31	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
32	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
33	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
34	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
35	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
36	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
37	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
38	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
39	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
40	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
41	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
42	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
43	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
44	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1
45	236	61.1	777	4	US-08-764 870 13	Sequence 15, Appl 1

```

RESULT 1
US-08-836-620A-15
Sequence 15, Application US-08-836-620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 15
SEQUENCE TYPE: Nucleic Acid
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS
SOFTWARE: FASTA 2.0
CURRENT APPLICATION DATA:
AFI: 0411-0, NUMBER: 04-09, PDB: 620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607592.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORGANISM: Homo sapiens
US-08-836-620A-15
Query Match 100.0% Score 486 DB 25 Length 484
Post local similarity 100.0% Pred. No. 6, 1e-37
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0
1 CAVSSTVASTVHYGVWWSQV 65
|||||
65 CAVSSTVASTVHYGVWWSQV 65
|||||
61 CYEVMG 66
|||||

```



US-08-836-620A-5  
Sequence 5: Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08-836-620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP 96/06933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 485 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
US-08-836-620A-5

Query Match 99.28; Score 383; DB 2; Length 485;  
Best Local Similarity 98.58; Pred. No. 1,76-16;  
Matches 65; Conservative 1; Mismatches 0; Indels 0; Gaps 0.  
QY 1 CAVCSQVASTYHYVWSSCTKAFKRSISGHNITCPAINCTIRKPKRSQVATLTK 60  
DB 104 CAVCSQVASTYHYVWSSCTKAFKRSISGHNITCPAINCTIRKPKRSQVATLTK 163  
QY 61 CYEWGM 66  
DB 164 CYEWGM 169  
RESULT 6  
US-08-836-620A-11  
Sequence 11: Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08-836-620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP 96/06933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-836-620A-11

Query Match 98.78; Score 381; DB 2; Length 66;  
Best Local Similarity 98.58; Pred. No. 3,56-37;  
Matches 65; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAVCSQVASTYHYVWSSCTKAFKRSISGHNITCPAINCTIRKPKRSQVATLTK 60  
DB 1 CAVCSQVASTYHYVWSSCTKAFKRSISGHNITCPAINCTIRKPKRSQVATLTK 60  
QY 61 CYEWGM 66  
DB 61 CYEWGM 66

RESULT 7  
US-08-836-620A-13  
Sequence 13: Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08-836-620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP 96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 484 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-836-620A-13

Query Match 98.78; Score 381; DB 2; Length 484;





```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-4061
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: protein
US-09-041-886-35

Query Match          98.48; SCORE 380; DR 4; length 595;
Best Local Similarity 97.93; Pred. No. 4,86-46;
Matches 64, Conservative 2, Mismatches 0; Indels 0; Gaps 0;

CY      1  GAVSEVASYRHWSTSTFKATFESLSQNYLTATSLTFPSTSYAELR 60
26      165  LAGVHVASVHWASLLTATREKLELDNRNMTATNLTTFSTFSTLATTF 144
CY      61  CYEVM 66
          11111
Db      245  CYEVM 250

RESULT 13
US-08-764-870-12
Sequence 12, Application US,08764870
Patent No. 6236946
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S
APPLICANT: Bayter, John D
APPLICANT: Fretterick, Robert J
APPLICANT: Wagner, Richard J
ATTORNEY: Kuschel, Peter J
APPLICANT: Applelie, James W
APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Cooley Godward
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13 DEC-1995
PRIOR APPLICATION DATA:

```









REGISTRATION NUMBER: 41,015  
 REFERENCE/WORK NUMBER: P-11 2626  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 546, 9001  
 TELEFAX: (619) 546, 9049  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 419 amino acids  
 TYPE: amino acid  
 PRIMARY: linear  
 MULTIPLE TYPE: protein  
 DEFINED BY: 006, 11

Query Match: 61.1% Score 249; Pos 4; Length 918  
 Best Local Similarity: 59.1% Pos 1 to 19; Indels: 0; Gaps: 0  
 Matches: 59; Conserved: 6; Mismatches: 19; Indels: 0; Gaps: 0

57 1 CAWSSYASGVYGVSWTQKAFKKSIGQINDYDATTNCTIDNKRKSVAKRKK 60  
 1 111 111 111 11 111111 11 11 1111111111 111111  
 10 508 CLTQGEASRGVGLVGSFVFKKAKKRGYTFVASNCTIDNKRKSVAKRKK 617  
 57 61 GYEVAM 66  
 10 619 GYEVAM 624

RESULT: 25  
 5/1/00/1  
 Patient No. 521767  
 APPLICANT: EVAN, E. NATHAN JR. LINDSEY, CLAREM M.  
 TITLE OF INVENTION: REVERSE TRANSCRIPTION  
 CHARACTERIZATION, IDENTIFICATION  
 NUMBER OF SEQUENCES: 4  
 CURRENT APPLICATION DATA:  
 FILING DATE: 05/07/2000, 614  
 FILING TO NO: 1  
 LENGTH: 66  
 5/1/00/1

Query Match: 61.1% Score 249; Pos 6; Length 66;  
 Best Local Similarity: 59.1% Pos 1 to 20; Indels: 0; Gaps: 0  
 Matches: 59; Conserved: 9; Mismatches: 18; Indels: 0; Gaps: 0

57 1 CAWSSYASGVYGVSWTQKAFKKSIGQINDYDATTNCTIDNKRKSVAKRKK 60  
 1 111 111 111 11 111111 11 11 1111111111 111111  
 10 1 CAWSSYASGVYGVSWTQKAFKKSIGQINDYDATTNCTIDNKRKSVAKRKK 69  
 57 61 GYEVAM 66  
 10 619 GYEVAM 624

RESULT: 27  
 US-08-087-151-3  
 Sequence: 3; Application US/0808/151  
 Patient No. 5468624  
 GENERAL INFORMATION:  
 APPLICANT: E. Brad Thompson  
 TITLE OF INVENTION: ACTIVE SITE ACTIVITY OF A MODIFIED FRAGMENT  
 NUMBER OF SEQUENCES: 4  
 CLASSIFICATION: 540  
 ADDRESS/AGENT INFORMATION:  
 ADDRESS: Arnold, White & Burke  
 STREET: P.O. Box 4434  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: pc dos/MS DOS  
 SOFTWARE: wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/087-151  
 FILING DATE: July 7, 1994  
 CLASSIFICATION: 435  
 ADDRESS/AGENT INFORMATION:  
 NAME: Hodgins, Daniel S.  
 REGISTRATION NUMBER: 41,026  
 REFERENCE/WORK NUMBER: 01-01, 141/100  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 512-320-7200  
 TELEFAX: 512-324-7577  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 89 amino acid residues  
 TYPE: amino acid  
 CHARACTERISTICS: single  
 PRIMARY: linear  
 MULTIPLE TYPE: protein  
 DEFINED BY: 08-087-151-3

Query Match: 61.1% Score 249; Pos 1; Length 89;  
 Best Local Similarity: 59.1% Pos 1 to 20; Indels: 0; Gaps: 0  
 Matches: 59; Conserved: 9; Mismatches: 18; Indels: 0; Gaps: 0

57 1 CAWSSYASGVYGVSWTQKAFKKSIGQINDYDATTNCTIDNKRKSVAKRKK 60  
 1 111 111 111 11 111111 11 11 1111111111 111111  
 10 2 CAWSSYASGVYGVSWTQKAFKKSIGQINDYDATTNCTIDNKRKSVAKRKK 69  
 57 61 GYEVAM 66  
 10 84 GYEVAM 89

RESULT: 28  
 US-08-061-072-3  
 Sequence: 3; Application US/0806/072  
 Patient No. 5571791  
 GENERAL INFORMATION:  
 APPLICANT: E. Brad Thompson  
 TITLE OF INVENTION: ACTIVE SITE ACTIVITY OF A MODIFIED FRAGMENT  
 NUMBER OF SEQUENCES: 4  
 ADDRESS/AGENT INFORMATION:  
 ADDRESS: Arnold, White & Burke  
 STREET: P.O. Box 4434  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: pc dos/MS DOS  
 SOFTWARE: wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/061-072  
 FILING DATE: 20-Nov-1995  
 CLASSIFICATION: 540  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/061-151  
 FILING DATE: July 7, 1994  
 ADDRESS/AGENT INFORMATION:  
 NAME: Hodgins, Daniel S.  
 REGISTRATION NUMBER: 41,026  
 REFERENCE/WORK NUMBER: 01-01, 141/100  
 TELECOMMUNICATION INFORMATION:



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[illegible]

	18-78	Score 221	18-2	Leath A10
Percent Match	18.78			
Percent Similarity	41.6%			
Matches	6M			
Conservative	34			
Mismatches	97			
Indels	18			
Gaps	5			

SKINAFLEASPOONSTILEA WITH VITAMIN E AND VITAMIN C POWDER  
SCIENTIFIC INFORMATION ON SKINAFLEASPOONSTILEA WITH VITAMIN E AND VITAMIN C POWDER

76. LAMONTAGNI ET AL.: VITAMIN D AND VITAMIN E IN THE PREVENTION OF  
 261. LAMONTAGNI ET AL.: VITAMIN D AND VITAMIN E IN THE PREVENTION OF  
 261. LAMONTAGNI ET AL.: VITAMIN D AND VITAMIN E IN THE PREVENTION OF

[illegible]

195 LSHPHASBP-30PRT-NMR-KRVVYVDT-FM-MA-200  
| : | ||| | : ||||  
470 LFAKSLGKLEHLPFKLGDPTDFTMEMLEA 405

287

11-2 reagent 11 binding protein - mouse (11 reagent)

# Date: 15-Jun-1990 # Sequence\_revision 09-Oct-1992 # text\_change 20-Sep-1999  
 # Accession: A14418

Kellamada, K.; Oleson, S. L.; Levi, B. Z.; Hirschfeld, S.; Appella, E.; Ozato, K.

Contract grant sponsor: National Institutes of Health, contract grant number: A-4418; NIH: 40045782.

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WILLIAMS, J. S. - [1946] - HAM-

the Zingales family, investigated ortho related proteins: ortho transforming protein

Cellular Transformation of Prostate Epithelial Cells by EBNA-2 and EBNA-5

— — — — —

best local similarity 41.58; Pred. No. 1.4e-12.

16. SRI SAMPALHA SMMSTRI ADEKI YIMTSWAKK I P'ETVEI SI FIVVRI I ES'WMEVI MM? 75

[illegible][illegible]

RESULT 29  
1041727  
retinoid X receptor beta - mouse

CiDate: 31-Dec-1998 #suppooe\_position 31 Dec 1998 #owl\_chhno 17 Mar 1999  
 #Aposposo p41227  
 Field, H., Kistner, P., Myers, R., Mubshari, H., Saunders, M., Zaslavsksk

Author: P. F. J. VAN DER KAM, and J. R. H. VAN DER KAM  
 A.Reference number: A41727; MD11:9212755  
 A.Accession: D41727

A: Molecule type: mRNA  
A: Residues: 1-448, 1H1  
A: Experimental source: liver

C: Genomes:  
A: Start codon: CUG  
C: Superfamily: unassigned erba-related proteins: erba-trans

**F118-364/Domain: etla transforming protein homologs - ETRA**

Post Local Similarity: 31.56; Pred. No. 1.4e-12;  
Mat. No. 75; Observed at 97; Models: 16; Caps:

DB 245 SSPNPVT - - - - - NICGAIKULFTLVMAKRIPIHPSNIPIDYVILAKAGWELLTAS 298

299 FSHFSINWVRLSILALGLHYHNSAISA-GVAAIFLPVLTETVSKMPIMBMOKIHDGTLK 357

458 ALLEMPIAKKI ..... SNIPHEVILPERVASYITY Keskylä 407

DE 408 LPALRSTLTKLPHLEPKLIGDIPDILMEMLEA 445

### RESULT 30

#### A41651

#### retinoic acid receptor coregulator - rat

[illegible]

Cell 1672, 1231 (2006), 1994  
A title, ESRbet, a catalyst that enhances binding of retinoic acid, thyroid hormone  
A reference number: A41651; MUID:92104690  
A Accession: A41651

A-Seedust; Preliminary  
A-Melonsilo type; mRNA  
A-Restides; 1-451 SYUA  
A-Crossed; 0.070895 CB-MB1766  
M114-296632; PIN-AA432511; M114-296634

Cellular family: unknown (EDA-related proteins) (EDA-transformed protein homolog)

